

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 23:00:34 ; Search time 4117 Seconds  
(without alignments)  
10274.813 Million cell updates/sec

Title: US-10-612-379-1  
Perfect score: 873  
Sequence: 1 atggcagaagttaccagat.....ccgatgttaatttcattaa 873

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	873	100.0	873	3	AY308063 Caenorhab
2	381	43.6	110000	2	Continuation (3 of
3	381	43.6	277607	3	CEY105E8A
4	279	32.0	24174	3	CBRG35I24
5	238.4	27.3	110000	2	CEY105E8_3
6	76.4	8.8	1063	6	CQ595182 Sequence
7	76.4	8.8	1090	6	AR521207 Sequence
8	76.4	8.8	1384	3	AY058721 Drosophil
9	76.4	8.8	1880	6	AR505752 Sequence
10	51.2	5.9	2000	6	AX655393 Sequence
11	48	5.5	877	9	CRS333501 Homo sapi
12	48	5.5	944	9	BC012444 Homo sapi
13	48	5.5	999	9	AF097330 Homo sapi
14	48	5.5	2238	3	AX833868 Sequence
15	48	5.5	2238	9	AK095959 Homo sapi
16	47.6	5.5	28057	3	CEP26111 Caenorhabdi
17	47.4	5.4	7218	6	I66494 Sequence 14
18	47.2	5.4	450	6	CQ721554 Sequence
19	46.4	5.3	819	6	AR149778 Sequence

20	46.4	5.3	819	6	BD190878 Human ani
21	46.4	5.3	819	6	AR271589 Sequence
22	45.4	5.2	1397	5	BC076239 Danio rer
23	44.8	5.1	1633	9	AF109196 Homo sapi
24	44.6	5.1	95660	2	AC131181 Homo sapi
25	44.6	5.1	107755	9	AC116628 Homo sapi
26	44.6	5.1	156817	9	AC009406 Homo sapi
27	43.4	5.0	842	6	CQ716785 Sequence
28	43.4	5.0	1229	6	BD094065 Shear str
29	43.4	5.0	1229	9	HSP64BCCP
30	43.4	5.0	1604	9	BC022305 Homo sapien
31	43.4	5.0	1640	9	BC005367 Homo sapi
32	43.4	5.0	1652	6	AR339324 Sequence
33	43.4	5.0	1722	6	CQ491450 Sequence
34	43.4	5.0	1722	6	CQ497331 Sequence
35	43	4.9	10560	6	CQ595181 Sequence
36	43	4.9	44319	2	AC013191 Drosophil
37	43	4.9	92969	2	AC010844 Drosophil
38	43	4.9	142372	9	AC132152 Homo sapi
39	43	4.9	168384	3	AC011069 Drosophil
40	43	4.9	209320	2	AC060776 Homo sapi
41	43	4.9	217422	9	AC108721 Homo sapi
42	43	4.9	307761	3	AE003493 Drosophil
43	42.8	4.9	447	9	AF426169 Homo sapi
44	42.8	4.9	511	4	AF109198 Bos tauru
45	42.8	4.9	859	6	AX921765 Sequence

## ALIGNMENTS

RESULT 1  
AY308063  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AY308063  
Caenorhabditis elegans EXC-4 (exc-4) mRNA, complete cds.  
AY308063  
AY308063.1 GI:34559858  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (Bases 1 to 873)  
Berry, K.L., Bulow, H.E., Hall, D.H. and Hobert, O.  
A Caenorhabditis elegans CLIC-like protein required for intracellular tube formation and maintenance  
Science (2003) In press  
2 (Bases 1 to 873)  
Berry, K. and Hobert, O.  
Direct Submission  
Submitted (27-MAY-2003) Biochemistry, Columbia University, 701 W.168th St., New York, NY 10032, USA

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/db\_xref="taxon:6239"  
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NRVEQLSNIDQLLSERKSYLLGNSTMEYDCELMPLRHIRIIGLSLLGDFDPNFT  
HLWAYITAYRTAAPIESCQADQDIHHYKEQMNLFNTQRETLPQSPKTKHTIPEKVL  
DIRVKGAPDVNVH"

ORIGIN



dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.  
**IMPORTANT:** This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

For a graphical representation of this sequence and its analysis see:- <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Y105E8A>

For a graphical representation of this sequence and its analysis see:- <http://>

**IMPORTANT:** This sequence is not the entire insert of clone Y105E8A. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone Y54E5 is at 356131 in this sequence. The true right end of clone F49B2 is at 104 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence Z81543. The end of this sequence (277504..277607) overlaps with the start of sequence A1132877.

#### FEATURES

##### Location/Qualifiers

1..277607

/organism="Caenorhabditis elegans"

/mol\_type="genomic DNA"

/strain="Bristol N2"

/db\_xref="taxon:6239"

/chromosome="I"

/clone="Y105E8A"

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10412..10645))

/gene="Y105E8A.1"

complement(join(8762..8781,8884..8953,9025..9099,

10412..10645))

/gene="Y105E8A.1"

/standard\_name="Y105E8A.1"

/note="contains similarity to Pfam domain PF04908

(SH3-binding, glutamic acid-rich protein)"

/codon\_start=1

/product="Hypothetical protein Y105E8A.1"

/protein\_id="CAB60842.2"

/db\_xref="GI:38422775"

/db\_xref="UniProt/TREMBL:Q9NF23"

/translation="MAPKVIVASATANPETKRYRVQRTLMILDGIGIFPDSIDITKPE  
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21844..22457,24788..25147))

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 IKDPLTGTNTELSDDVVRNKNRFLCKLQIDVEVKNVYSGATAGKLETM  
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 QVKPATRIENEDPYYSVSNHYGSCDVGTGKPTTDVVYICVEKQHKLSVTEIS  
 SCHYEVIMTDLCKHPEVQLSEKKDKIKVCWNEAKNEAKPTQLRLDDHDSLF  
 KRYVFTDQDPQISENTEEDDGLIDKDFEKLKTRQAGYILGQVKRFTKESLAN  
 NPAVVHTNRILTGEDCIVGGTGMWKYFCYGRHVIQFHEDANGQRSDILLGVFDE  
 VHKWVMDRARGAIOQNGNIDISQIYAKGIDCEGTGAHNVEVRIKCATADHSALS  
 FSHMTBPTCOYVLTIIDISERFCEPLQFADYDGLTELQVASSQSAAAAAA  
 VEELS  
 IDEEDBAHQSDDBDDHVKIHEDL"

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27768..28086,29660..30045,31473..31976,33263..33496,

34152..34244)

/gene="Y105E8A.3"

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 34152..34244)  
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 /standard\_name="Y105E8A.3"  
 /note="contains similarity to Pfam domain PF01545 (Cation  
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/protein\_id="CAD21657.2"

/db\_xref="GI:24817580"

/db\_xref="GOA:Q8WQB6"

/db\_xref="UniProt/TREMBL:Q8WQB6"

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 DRCITLQCPILSRVLVFLSLSTVLSAVSVFSGKGNMSPKTRGFLVIGFVALFLM  
 PDGCTIDPHHTTHAHSLGNLHVHLIGLFGMDHKGGLCTILLILSLTRGVTSEFR  
 HLAVEGGAKLHLTVTAGSAVCLTPVAVLSWALSSSSGASIGYFHYAALLVIAVAV  
 FVLDFYAESICFQHVADPVMARWSSVMFSCAPFLAYLWYQNLGDHALTGGVSI  
 TVVCFILASISLTHSNQPKRRGHFVIGISNTGLPLFTYGEAFLQRTSKSLMFKETL  
 NEILMNDSRRIFWFLCVNLGFCGVFLYGFWTNSLGLISDGFHMLFDCSALVMGLVA  
 SVMARWPTRHPTFGFGRVEILSGFINALFLCVIALFLIEALERLFPDPNINTORLL  
 FVAISGLIVNLFGMYSLGEHCHSHGGSHGGSHGGSHGGSHGGSHGGSHGGVPLH  
 VLADTSLGVFVLIITLLIQWFGWVNDPLCSLILSLIIIGSVYPLLVSSISITLQDVP  
 EEEFEYHINEIIEIHVESYNAHMQHSDINVASVHVQVKEANAQMIKRRVSNII  
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/standard\_name="Y105E8A.4"

/note="contains similarity to Pfam domain PF00378

(Enoyl-CoA hydratase/isomerase)"

/codon\_start=1

/product="Hypothetical protein Y105E8A.4"

/protein\_id="CAC48118.1"

/db\_xref="GI:15130766"

/db\_xref="GOA:Q9NEZ8"

/db\_xref="UniProt/TREMBL:Q9NEZ8"

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 FALGQAEALMCDIVYAGNAIFGQPEITITIGLGTQFMRPVYKRSVAMEICLS  
 GDRIGAQAEKEDGLSVKVPVQVLQGEAVLLADRIAKNSPLIVTKVKSLSAYQTSLS  
 NQGLEMRKQLFQSTFATNDRREGMSFAEKAEPKWTSS"

#### gene

complement(join(38162..38414,39163..39338,39389..39748,

40251..40334,40489..40628,40809..40974,41025..41246,

41384..41458,42603..42857))

/gene="Y105E8A.5"

complement(join(38162..38414,39163..39338,39389..39748,

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41384..41458,42603..42857))

/gene="Y105E8A.5"

/standard\_name="Y105E8A.5"

/note="C. elegans BBS-1 protein; contains similarity to

Red clover mottle virus Genome polyprotein B [Contains:

Protease cofactor; Membrane binding protein; VPg; Protease

(EC 3.4.22.-); RNA polymerase (EC 2.7.7.48)].;

SW:VGNB\_RCNW"

/codon\_start=1

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/db\_xref="GI:15130767"

/db\_xref="UniProt/TREMBL:Q9NEZ7"

/translation="MAKPVNVNQSKWTVPVLLKCEYICPSTCVAFGPILSDNSDKLI  
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 KNLKPFYKTPSSAINTPTESEAWKAVKNKINGDTLLTKRLDEVDVFKSLTPIQS  
 TYLRADKETQVLVHYHTKIANGATITIAKLTSTAEPLDILVIGTEHCEIFLIDS  
 QAFITLTIKGISVFNICAYQTDVDFVQTRASLFCWKREADYQPTIVIQSQM  
 ITSVALNKMIVVTTVENIHFASPRGKMNTVKCPSKI KMLEPPIYPLKOLAAVAV  
 FDKIRMYNEHLDTVQYKPLAWKYGCYGREDSITLVAFKDGSIATQIFRRKANF  
 DTLDYQVPOAHALKQIPKKTVDLTGTREVOLGNRIKHLFSDQVDFVYRLAAS  
 YLELTSSASATVSTTTTLPVLPVEISVDIHGFTFRMTHTLLSSSKQNLDMHLIISDP



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Matches 248; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 503 CCAATATTGATCAGTGTCTATCCGAGAGAAAATCTCGATATCTACTTGGAAACAGATATGA 562
Db 15738 CCATTTATTGCGATTGCTATCCGAGAGAAAATCTCGATATCTACTTGGAAACAGATATGA 15797
QY 563 CTGAATATGACTGTGAACCTGATGCGACGCTTTCATCATATTCGAATATTTGGAATGTCAC 622
Db 15798 CTGAATATGACTGTGAACCTGATGCGACGCTTTCATCATATTCGAATATTTGGAATGTCAC 15857
QY 623 TTCTTGGATTTCGATATTCACATAATTTTCACTCATCTCTGGGCTTATATCCTCACTGCA 682
Db 15858 TTCTTGGATTTCGATATTCACATAATTTTCACTCATCTCTGGGCTTATATCCTCACTGCA 15917
QY 683 ACCGTACAGCAGCATTTATTGAGAGTTGTCCGCGCATCAGACATTTATTCATCACTATA 742
Db 15918 ACCGTACAGCAGCATTTATTGAGAGTTGTCCGCGCATCAGACATTTATTCATCACTATA 15977
QY 743 AAGAACAAATGAATCTGTTCAAA 766
Db 15978 AAGTGAGGATGAAGCTGCAAACTA 16001

RESULT 6
LOCUS CQ595182 1063 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 22940 from Patent WO0171042.
ACCESSION CQ595182
VERSION CQ595182.1 GI:41652101
KEYWORDS Drosophila sp.
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
REFERENCE Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
AUTHORS Detection kits, such as nucleic acid arrays, for detecting the
TITLE expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL Patent: WO 0171042-A 22940 27-SEP-2001;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:7242"

ORIGIN
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Best Local Similarity 52.5%; Pred. No. 4.1e-09;
Matches 167; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
QY 495 GCAACTATCCATATTTGATCAGTGTCTATCCGAGAGAAAATCTCGATATCTACTTGGAAA 554
Db 727 GCATCTGCGCAAGATCAACGATCATCTGTCCGCGGCAACACGCGCTTCTCCACCGCGGA 786
QY 555 CAGTATGACTGAATGATGCTGGAATGATGCGACGCTTTCATCATATTCGAATATTTGG 614
Db 787 CACCATGTGCTCTCGACTGTGAGCTGATGCGCGCTGCGAGCATCCGTTGGCGGG 846
QY 615 ATTGTCACTTTTGGATTGATATTCACATAATTTCACTATCTCTGGGCTTATATCCT 674
Db 847 CAAGTACTTTTGCAGCTTTGAAATCCCGACGCACTTGACGGCCCTGTGGCGCTACATGTA 906
QY 675 CACTGCATACCGTACAGCAGCATTTTTCAGAGATTTGTCGCGCGATCAGGACATTTTCA 734
Db 907 TCATATGATACAGCTGGAGCGCTTTCACAAATCTGTCGCGCGGCGGACGAGCATTTCAA 966
QY 735 TCACATATAAGAAACAAATGAATCTGTTCACAAATCAACGTGAAACCTCCCAATCCGCAAC 794
Db 967 TCACATACAGCTGCAACAGAGTCTCAAAATGAAGAGCAGCAGGAGCTGGAGACGCCAC 1026
QY 795 AAAAAACGCACACAATTC 812
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Db 1027 GTTTACCACATACATTC 1044
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RESULT 7
LOCUS AR521207 1090 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 26167 from patent US 6703491.
ACCESSION AR521207
VERSION AR521207.1 GI:52456682
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1090)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 26167 09-MAR-2004;
FEATURES
source Location/Qualifiers
1..1090
/mol_type="genomic DNA"

ORIGIN
Query Match 8.8%; Score 76.4; DB 6; Length 1090;
Best Local Similarity 52.5%; Pred. No. 4.1e-09;
Matches 167; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
QY 495 GCAACTATCCATATTTGATCAGTGTCTATCCGAGAGAAAATCTCGATATCTACTTGGAAA 554
Db 28 GCATCTGCGCAAGATCAACGATCATCTGTCCGCGGCAACACGCGCTTCTCCACCGCGGA 87
QY 555 CAGTATGACTGAATGATGCTGGAATGATGCGACGCTTTCATCATATTCGAATATTTGG 614
Db 88 CACCATGTGCTCTCGACTGTGAGCTGATGCGCGCTGCGAGCATCCGTTGGCGGG 147
QY 615 ATTGTCACTTTTGGATTGATATTCACATAATTTCACTATCTCTGGGCTTATATCCT 674
Db 148 CAAGTACTTTTGCAGCTTTGAAATCCCGACGCACTTGACGGCCCTGTGGCGCTACATGTA 207
QY 675 CACTGCATACCGTACAGCAGCATTTTTCAGAGATTTGTCGCGCGATCAGGACATTTTCA 734
Db 208 TCATATGATACAGCTGGAGCGCTTTCACAAATCTGTCGCGCGGCGGACGAGCATTTCAA 267
QY 735 TCACATATAAGAAACAAATGAATCTGTTCACAAATCAACGTGAAACCTCCCAATCCGCAAC 794
Db 268 TCATATACAGCTGCAACAGAGTCTCAAAATGAAGAGCAGCAGGAGCTGGAGACGCCAC 327
QY 795 AAAAAACGCACACAATTC 812
Db 328 GTTTACCACATACATTC 345

RESULT 8
LOCUS AY058721 1384 bp mRNA linear INV 16-OCT-2001
DEFINITION Drosophila melanogaster LD46306 full length cDNA.
ACCESSION AY058721
VERSION AY058721.1 GI:16185714
KEYWORDS FLI CDNA.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
REFERENCE 1 (bases 1 to 1384)
AUTHORS Epiphytoida; Drosophilidae; Drosophila.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanavong,S., Wan,K.,
Yu,C., Lewis,S.E., Rubin,G.M. and Celnikier,S.
TITLE Direct Submission
```

Submitted (08-OCT-2001) Berkeley Drosophila Genome Project,  
Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, USA  
Sequence submitted by:  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to  
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,  
Science 2000). The sequence has been subjected to integrity checks  
for sequence accuracy, presence of a polyA tail and contiguity  
within 100 kb in the genome. Thus we believe the sequence to  
reflect accurately this particular cDNA clone. However, there are  
artifacts associated with the generation of cDNA clones that may  
have not been detected in our initial analyses such as internal  
priming, priming from contaminating genomic DNA, retained introns  
due to reverse transcription of unspliced precursor RNAs, and  
reverse transcriptase errors that result in single base changes.  
For further information about this sequence, including its location  
and relationship to other sequences, please visit our Web site  
(<http://fruitfly.berkeley.edu>) or send email to  
[cdna@fruitfly.berkeley.edu](mailto:cdna@fruitfly.berkeley.edu).

FEATURES		Location/Qualifiers	
Source	1. .1384	/organism="Drosophila melanogaster"	
		/mol_type="mRNA"	
		/strain="y; cn bw sp"	
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Gene	1. .1384	/genes="CG10997"	
		/notes="alignment with genomic scaffold AE003493"	
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		/protein_id="AAL13950.1"	
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ORIGIN			
Query Match	8.8%;	Score 76.4;	DB 3; Length 1384;
Best Local Similarity	52.5%;	Pred. No. 4e-09;	
Matches 167;	Conservative	0;	Mismatches 151; Indels 0; Gaps 0;
QY	495	GCAACTATCCAAATATTGATCAGTTGGTATCCGAGAGAAATCTCGATATCTACTTGGAAA	554
Db	763	GCATCTCGCAAGATCAACGATCATCTGTCCGCGCGCAACACGCGTCTCTCACCGCGCA	822
QY	555	CAGTATGACTGAATATGATGCTGCAACTGATGCCAGCTTTCATCATATTGCAATTATTGG	614
Db	823	CACCATGTCGCTTTCGATGTGAGCTGATGCGCGCCTGCGAGCACATCCGTGTGCGCGG	882
QY	615	ATTGTCACATCTTTGGATTTCGATATCCACATAATTTCACTCATCTCTGGGCTTATATCTCT	674
Db	883	CAAGTACTTTTTCGACTTTTGAATCCGACGCACTTGACGGCCCTGTGGCGGTACATGTA	942
QY	675	CACTGCATACCGTACAGCAGCATTTATTGAGAGTTGTGCCGCGGATCAGGACATTATCCA	734
Db	943	TCACATGTACCAAGCTGGAGCGCTTCCACAATCGTCCCGCGCGCACGAGCATTAATCAA	1002
QY	735	TCACATATAAGAACAAATCAATCTGTTTCCAAATCAACGTGAACCCCTCCAATCGCCAC	794
Db	1003	TCATCTACAGCTGCAACAGAGTCTCAAAATGAAGACGACGAGGAGCTGGAGCGCCAC	1062
QY	795	AAAAACGCACAAATTC	812

Db	1063 GTTTACCACATACATTCC 1080	
RESULT 9		
AR505752	AR505752	1880 bp DNA linear PAT 22-SEP-2004
LOCUS	Sequence 10712 from patent us 6703491.	
DEFINITION	AR505752	
ACCESSION	AR505752.1	GI:52441227
VERSION		
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 1880)	
AUTHORS	Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L., Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.	
TITLE	Drosophila sequences	
JOURNAL	Patent: US 6703491-A 10712 09-MAR-2004;	
FEATURES	Location/Qualifiers	
source	1..1880	
	/organism="unknown"	
ORIGIN	/mol_type="genomic DNA"	
Query Match	8.9%; Score 76.4; DB 6; Length 1880;	
Best Local Similarity	52.5%; Pred. No. 4e-09;	
Matches 167; Conservative	0; Mismatches 151; Indels 0; Gaps 0;	
Qy	495 GCAACTATCCAAATTGATCAGTTGCTATCCGAGAGAAATCTCGATATCTACTTGGAAA	554
Db	818 GCATCTGCGCAAGATCAACGATCATCTGTCCGCGCCACACGGGTTCTCACCGGCGA	877
Qy	555 CAGTATGACTGAATATGACTGTGAACTGATGCGACAGTCTTTTCATCATATTCGAATTATGG	614
Db	878 CACCATGTGCTGTCTCGACTGTGAGCTGATGCGCGCCTCCAGCACATCCGTGTGGCGG	937
Qy	615 ATTGTCACTTCTTGGATTTCGATATCCACATAATTTCACTCATCTCTGGGCTTATATCCT	674
Db	938 CAGTACTTTGTCGACTTTGAAATCCGAGGCACTTGACGGCCTGTGGCGTACATGTA	997
Qy	675 CACTGCATACCGPACAGCAGCAATTTATTGAGAGTTGTCCCGCGCATCAGGACATTATCA	734
Db	998 TCACATGTACCACTGGAGCGCTTCCACAAATCGTCCCGCGCCAGCAGGACATTATCAA	1057
Qy	735 TCACATAAGACAAATCAATCTGTTTCAAAATCAAGTGAAACCTTCATCCGCCAAC	794
Db	1058 TCACTACAGCTGCAACAGAGTCTCAAATGAAGACGACGAGGAGCTGGAGACGCCAC	1117
Qy	795 AMAACGCGACACAATTC 812	
Db	1118 GTTTACCACATACATTCC 1135	
RESULT 10		
AR655393/c	AR655393	2000 bp DNA linear PAT 22-MAR-2003
LOCUS	Sequence 5263 from Patent WO0300098.	
DEFINITION	AR655393	
ACCESSION	AR655393.1	GI:29158207
VERSION		
KEYWORDS	Oryza sativa	
SOURCE	Oryza sativa	
ORGANISM	Oryza sativa	
REFERENCE	1	
AUTHORS	Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.	
TITLE	Plant genes involved in defense against pathogens	
JOURNAL	Patent: WO 0300098-A 5263 03-JAN-2003;	
FEATURES	Syngenta Participations AG (CH)	
	Location/Qualifiers	



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QY 720 TCAGGACATTATTTCATCATATAAAGACAACAATGATCTGTTCCACAATCAA 771
Db 711 TAAGGAGGTGAATAGCATATAGTGTAGTACCAAAAGAGACTCACCAGTAA 762

RESULT 12
BC012444 944 bp mRNA linear PRI 29-JUN-2004
LOCUS Homo sapiens chloride intracellular channel 4, mRNA (cDNA clone
DEFINITION MGC:8812 IMAGE:3861372), complete cds.
ACCESSION BC012444
VERSION BC012444.1 GI:15214635
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 944)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shermen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeb, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Diatchenko, L., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gumaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 944)
Straussberg, R.
Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue procurement: DCTD/DP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgobcm.tmc.edu
Guanarane, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 21 Row: f Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7330334.
Location/Qualifiers
1. 944
/organism="Homo sapiens"
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REMARK COMMENT
SOURCE source
FEATURES

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Best Local Similarity 50.4%; Pred. No. 0.13;
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
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QY 600 TATTCGAATTATTGGATGTGCCTCTTGGATTGCATATTCACATATTTCACTCATCT 659
Db 741 TGTCAAGGTGGTGGCCAAAATAATCGCACTTTGATATATCCAAAGAAATGACTGCAT 800
QY 660 CTGGCTTATATCTCTACTGCATACCGTACAGAGCATTTATTGAGAGTTGTCCGCCGA 719
Db 801 CTGGAGATACCTAACTAATGATACATAGTAGGAGGAGTTCCACCAATACCTGTCCAGTGA 860
QY 720 TCAGGACATTATTTCATCATATAAAGACAACAATGATCTGTTCCACAATCAA 771
Db 861 TAAGGAGGTGAATAGCATATAGTGTAGTACCAAAAGAGACTCACCAGTAA 912

RESULT 13
AF097330 999 bp mRNA linear PRI 14-JUN-1999
LOCUS Homo sapiens H1 chloride channel mRNA, complete cds.
DEFINITION AF097330
ACCESSION AF097330.1 GI:5052201
VERSION AF097330.1
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 999)
Edwards, J.C.
TITLE A novel p64-related Cl- channel: subcellular distribution and
nephron segment-specific expression
Am. J. Physiol. 276 (3 Pt 2), F398-F408 (1999)
JOURNAL 99170604
MEDLINE 10070163
PUBMED 2 (bases 1 to 999)
REFERENCE Edwards, J.C.
AUTHORS Direct Submission
TITLE Submitted (05-OCT-1998) Medicine, Washington University, 216 S.
JOURNAL Kinghighway, St. Louis, MO 63110, USA
FEATURES Location/Qualifiers
1. 999
/organism="Homo sapiens"
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ORIGIN
Query Match      5.5%; Score 48; DB 9; Length 999;
Best Local Similarity 50.4%; Pred. No. 0.13;
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 540 ATATCTACTTGGAAACAGTATGACTGAATATGACTGTGAACCTGTGCCACGCTTTCATCA 599
DB 671 ATTTCTGGATGCAATGAATGACATTAGCTGATTGCAACCTGTGCCAACCTGCATAT 730

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QY 660 CTGGCTTTATCTCTCACTGCGATACCGTACGACGACATTTATGAGAGTTGTCGCCGGA 719
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QY 720 TCAGGACATTTATTCATCACTATAAAGAACAAATGAATCTGTTCACAAAATCAA 771
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RESULT 14
AX833868
LOCUS
DEFINITION
Sequence 992 from Patent EP1347046.
ACCESSION
AX833868
VERSION
AX833868.1 GI:39920003
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

REFERENCE
AUTHORS
Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE
Full-length cDNA sequences
JOURNAL
Patent: EP 1347046-A 992 24-SBP-2003;
Research Association for Biotechnology (Jp)
FEATURES
Location/Qualifiers
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Best Local Similarity 50.4%; Pred. No. 0.12;
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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QY 600 TATTCGAATATTGGAATGTCTCTTGGATTCGATATTCACATATTTTCACATCTCT 659
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DB 851 TAAGGAGGTGGAATAGCATATAGTGATCGACCAAAAGACTCACCAAGTAA 902
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Db 697 TGTCAAGGTGGTGGCCAAAATAATCGCAACTTTGATATTCAAAAGAAATGACTGGCAT 756
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DB 817 TAAGGAGGTGGAATAGCATATAGTGATGTAGCACAAGAGACTCACCAAGTAA 868

RESULT 15
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LOCUS
DEFINITION
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to CHLORIDE INTRACELLULAR CHANNEL PROTEIN 4.
ACCESSION
AK095959
VERSION
AK095959.1 GI:21755327
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

REFERENCE
AUTHORS
Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
Wakamatsu,A., Hayaashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
Kikkawa,E., Omura,Y., Abe,K., Kamiyama,K., Katsuta,N., Sato,K.,
Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,
Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,
Hara,H., Tanase,T., Nomura,Y., Kanehori,K., Takahashi-Fujii,A.,
Yasuda,M., Houchi,T., Kusano,Y., Kanehori,K., Komai,F., Hara,R.,
Hirao,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N.,
Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T.,
Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togaishi,T.,
Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamaashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano.S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

2

Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamaashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
Unpublished
NEDO human cDNA sequencing project
3 (bases 1 to 2238)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kasuga-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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9342.172 Million cell updates/sec

Title: US-10-612-379-1

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	234.4	28.8	556	CD419508	rjllf07.y
5	229.4	26.3	599	CB375433	rw06g06.y
6	209.4	24.0	671	BF400411	SMOV3MCM
7	203.6	23.3	567	BE029008	kp23f02.y
8	202	23.1	483	A1043403	BSBMMFSZ0
9	189	21.6	566	CK242284	rx08a04.y
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30	76.4	8.8	403	7	CO273757	CR533981
31	74.4	8.5	572	8	BH761266	BM643363
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33	71.2	8.2	444	7	CO156493	EN08162.y
34	70.8	8.1	604	8	BH761283	BM643363
35	70.6	8.1	924	6	CD779293	EST50654
36	69.8	8.0	909	6	CD794560	EST50654
37	67.4	7.7	207	6	CA868922	pw91g05.y
38	66.6	7.6	706	4	BM587858	170006873
39	66.6	7.6	754	5	BM623011	BM623011
40	65	7.4	739	5	BM625406	BM625406
41	63.6	7.3	828	6	CD791336	EST50654
42	62.8	7.2	598	7	CO279118	EST50654
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
BQ548091 701 bp mRNA linear EST 17-JUN-2002  
rd20a06.y1 Meloidogyne incognita egg SL1 TOPO vi Meloidogyne  
incognita cDNA 5' similar to WP:CE25703 Y105E8C.A ; contains Alu  
repetitive element; mRNA sequence.  
ACCESSION  
BQ548091  
VERSION  
BQ548091.1 GI:21432594  
KEYWORDS  
EST.  
SOURCE  
Meloidogyne incognita (southern root-knot nematode)  
ORGANISM  
Meloidogyne incognita  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
REFERENCE  
1 (bases 1 to 701)  
McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,  
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R., and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
The library was constructed by Claire Murphy and Dr. James McCarter  
at Washington University, St. Louis. Meloidogyne incognita eggs  
were provided by Andrew Kloeck of Divergence Inc., St. Louis, MO.  
Seq primer: -40Rp from Gibco  
High quality sequence stop: 534.

TITLE  
JOURNAL  
COMMENT

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/organism="Meloidogyne incognita"  
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/db\_xref="taxon:6306"  
/dev\_stage="egg"  
/lab\_host="DH10B (Invitrogen)"  
/clone\_lib="Meloidogyne incognita egg SL1 TOPO v1"  
/note="Vector: pCR11-TOPO (Invitrogen); Site 1: EcoRI;  
Site 2: EcoRI; The library was constructed by Claire  
Murphy and Dr. James McCarter at Washington University,  
St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR



QY 464 AGATTAAAGTTCACTACAAATCGAGTCTGTGAGCAACTATCAAAATTTGATCAGTTGCTAT 523  
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 Db 468 AAGTCGCTCATCGCACAGCAAAATGGTGTAGAACAGCTGCGGAATATAAATCAGTTGGTGG 527  
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 QY 524 CCGAG---AGAAATCTCGATATCTACTTGTGGAACAGTATGACTGAATATGACTGTGAAC 580  
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 QY 581 TGATGCCACGCTCTTCATCATATTCGAAATTTATGGATTGTCACTTCTTCGGATTTCGATATTC 640  
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 QY 701 TTGAGAGTGTCCCGCGATCAGGACATATTCATCATATAAGAAACAAATGAATCTGT 760  
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 Db 708 TCGAGTCGTGTCGCGCTGACCAGGACATTTCTCCACCATTTACAAGGAGCAACTAAACCTTA 767  
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 QY 761 TCACAAAT 768  
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 Db 768 GCATCGAT 775

RESULT 3  
 LOCUS BF718901  
 DEFINITION SWOV3MCAM58D06SK Onchocerca volvulus molting L3 larva cDNA  
 (SI96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAM58D06 5',  
 mRNA sequence.

ACCESSION BF718901  
 VERSION BF718901.1 GI:12019909  
 KEYWORDS EST.  
 SOURCE Onchocerca volvulus

ORGANISM Onchocerca volvulus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 Onchocercidae; Onchocerca.  
 1 (bases 1 to 759)  
 REFERENCE Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.  
 Genes expressed in molting L3 larvae of Onchocerca volvulus  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Steven A. Williams  
 COMMENT Molecular Parasitology

Smith College Department of Biological Sciences  
 Department of Biological Sciences, Clark Science Center, Smith  
 College, Northampton, MA, 01063, USA  
 Tel: 4135853826  
 Fax: 4135853786  
 Email: genome@smith.edu

Seq primer: pBluescript SK.

FEATURES  
 source

Location/Qualifiers

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 /mol\_type="mRNA"  
 /strain="Kumba, Cameroon"  
 /db\_xref="taxon:6282"  
 /clone="SWOV3MCAM58D06"  
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 /lab\_host="XLI-Blue MRF"  
 /clone\_lib="Onchocerca volvulus molting L3 larva cDNA  
 (SL96MLW-Ovml3)"

/note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2:  
 Xho I; Filarial nematode parasite of humans. Third-stage  
 larvae, L3, were isolated from infected black flies in  
 Cameroon (forest strain). The L3 were cultured in 20% FCS  
 in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in  
 culture. L3 of O. volvulus molt to fourth-stage larvae by  
 day 5 in culture. mRNA was isolated from approximately  
 6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3  
 in culture, and converted to double-stranded cDNA using  
 reverse transcriptase and oligo(dT) followed by RNase H

and DNA pol I. The library was constructed in the lambda  
 Uni-Zap XR vector and has 1 x 10E6 independent  
 recombinants and the average insert size is ~1200 bp. The  
 library was constructed by Sara Lustigman and Michelle  
 Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.  
 The library is available from Dr. Sara Lustigman (email:  
 slustigman@ybc.org)."

# ORIGIN

Query Match 32.5%; Score 283.8; DB 2; Length 759;  
 Best Local Similarity 68.9%; Pred. No. 1-4e-71;  
 Matches 450; Conservative 0; Mismatches 192; Indels 11; Gaps 4;  
 QY 46 AAACCTCTTCGAGCTCTACGTAAAGCGTCAAGAAATTTGATGCTCGCCGCAATTCGAGCC 105  
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 QY 106 GATCTTTCTGTGAGGAATTCGTGATGAGTTGATGCTCTTATGAGATTGGATTGCA 165  
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 Db 157 TGCTTGTGTTGTCAGGAATTTTGGATGGAACCTTTACGCTCTTTATGAGATTGGCGTTGT 216  
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 QY 166 CGAGTCGAAGTGAAGACTGTCAACGTGAATTTCTGAAGCATTTAAGAGAACTTTCTCCGA 225  
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 Db 217 CGAGTTGAAGTGAAGACAGTAACATCAATTTCTGAGCATTCMAAAGAGTTTCTCCGA 276  
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 QY 226 GCACAAACCCGATTTATGATTGAAGAGGAAAGAGCTGACATACATCATGATAATCGAGAG 285  
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 Db 334 ATCGAAGGACGCAATTTTTCATTTAGCGAAAGAGTTCAATGTGCCATTTGTTGAGAAAG 393  
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 Db 394 CCAGTGTGAGAAACGAATTTGAAAGTTGTACAGAAATTTCAAAATCTTTTGGCATCC 453  
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 Db 693 TCCGCTGAATCTACCTATTTCTTGGAACTATGTGTTGAATGCATCCCGTACCG 745  
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 LOCUS CD419508

DEFINITION CD419508  
 accession cdna 5' similar to WP:CE25711 Y105EBE.Y ;, mRNA sequence.

ACCESSION CD419508.1 GI:31325771  
 VERSION EST.  
 KEYWORDS Meloidogyne chitwoodi  
 SOURCE Meloidogyne chitwoodi  
 ORGANISM Meloidogyne chitwoodi

REFERENCE 1 (bases 1 to 556)  
 AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagarishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R., and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

# TITLE JOURNAL

## COMMENT

Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

The library was constructed by Claire Murphy and Dr. Makedonka  
Dautova at Washington University, St. Louis. The cDNA was made by  
using Dynabead oligo-dT priming (Dyna). PCR based library using a  
modified protocol from the SMART PCR cDNA Synthesis Kit from  
Clontech. Directionally cloned into the UDG sites of pAMP1.  
Meloiodogyne chitwoodi eggs were provided by Dr. David Bird at North  
Carolina State University, Raleigh, NC (david\_bird@ncsu.edu).  
Seq primer: T3 from Gibco.

## FEATURES source

Location/Qualifiers  
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/organism="Meloiodogyne chitwoodi"  
/mol\_type="mRNA"  
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/lab\_host="DH10B"  
/clone\_libs="Meloiodogyne chitwoodi egg pAMP1 v1"  
/note="Vector: pAMP1; Site 1: Not I; Site 2: Sal I; The  
library was constructed by Claire Murphy and Dr. Makedonka  
Dautova at Washington University, St. Louis. The cDNA was  
made by using Dynabead oligo-dT priming (Dyna). PCR based  
library using a modified protocol from the SMART PCR cDNA  
Synthesis Kit from Clontech. Directionally cloned into the  
UDG sites of pAMP1. Meloiodogyne chitwoodi eggs were  
provided by Dr. David Bird at North Carolina State  
University, Raleigh, NC (david\_bird@ncsu.edu)."

## ORIGIN

Query Match 26.8%; Score 234.4; DB 6; Length 556;  
Best Local Similarity 65.1%; Pred. No. 3.7e-57;  
Matches 362; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 207 TAAGAGAACTTTCTCGAGACACACACCGATTATGATTGAAGAGGAAAAGAGCTGAC 266  
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QY 267 ATACACTGATATCGAGAGATTGAGGACGGATCTTTTCATTTGGCAAGGAATTCATGT 326  
DB 61 CTATGCAGACACACGCGAAATTTGAACGTCGTATTTTCCATCTCTGTCAGGTTTAAATGT 120  
QY 327 TCCACTCTTTGAAAGAGTCCATCCGCTGAGAGAGATAGAGAACTTTGTACAGGAACCTT 386  
DB 121 TCCACTTTTGAAGAGATTGCAAGTTGAGAAACTATTCAAATCTTTATCTTAATTT 180  
QY 387 CAACCTGTTCTCGAGCAAAAGTAGAGTTTCGATAAGGGAAAAAGAGCCATCGAGAGT 446  
DB 181 CAAATCTTTTGTGAAGCAAAAAGGACATCATGACAAAGGCAAAAGACGCTAGTACAAT 240  
QY 447 TGAAGA---TCTCCAGCACAGATTAAAGTTTCACCTACACATCGAGTCTGTGAGCAACTATC 503  
DB 241 TGGAGAGGGTCTTCCACCACAGAGTGGGCAACTTCTCATTAATAAATTTGGAGCAATTTGGC 300  
QY 504 CAATATTGATCAGTTGCTATCCGAGAGAAAATCTGATATCTACTTTGTTGAAACAGATGAC 563  
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QY 564 TGAATATGACTGTGACTGATCGCCACGTCCTTCATCATATTTGCAATTTGATTTGTCACT 623  
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QY 624 TCTTGGATTGATATCCACATATTTTCACTCATCTCTGGGCTTATATCTCTCACTGCATA 683  
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QY 684 CCGTACAGCAGCAATTTATTTAGAGTCTTCCGCGCATCAGACAAATTTATCATCACTATAA 743  
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QY 744 AGAACAAATGAATCTG 759  
DB 541 GGAGCAATTAATTTG 556

## RESULT 5 CB375433

LOCUS rW06906.y1 Heterodera glycyines virgin female Heterodera glycyines  
DEFINITION cDNA 5' similar to WP:CE25703 Y105E8C.A ; mRNA sequence.

ACCESSION CB375433

VERSION CB375433.1 GI:29051812

KEYWORDS EST.

SOURCE Heterodera glycyines

ORGANISM Heterodera glycyines

REFERENCE 1 (bases 1 to 599)  
Heterodera glycyines  
Tylenchoidea; Heteroderidae; Chromadorea; Tylenchida; Tylenchina;

## AUTHORS

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagarishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R., and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

## TITLE

## JOURNAL

## COMMENT

Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This library was generated by cloning cDNAs directionally into  
Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI  
are at the 3'-end). The library was excised [now in pBluescript  
SK(+)] and normalized (Bonald et al 1996 Genome Research  
6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu),  
Iowa State University, Plant Pathology Department and Jeff  
McDermott (jpmcderm@iastate.edu).

Seq primer: -40RP from Gibco

High quality sequence stop: 450.

## FEATURES

### source

Location/Qualifiers

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/tissue\_type="whole organism"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Heterodera glycyines virgin female"

/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI;  
Site 2: EcoRI; This library was generated by cloning cDNAs  
directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI  
are at the 5'-end and T7/XhoI are at the 3'-end). The  
library was excised [now in pBluescript SK(+)] and  
normalized (Bonald et al 1996 Genome Research 6:791-806).

Library constructed by Thomas Baum (tbaum@iastate.edu),  
Iowa State University, Plant Pathology Department and Jeff  
McDermott (jpmcderm@iastate.edu)."

## ORIGIN

Query Match 26.3%; Score 229.4; DB 6; Length 599;

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Best Local Similarity 62.9%; Pred. No. 1.1e-55;
Matches 372; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

QY 44 CAAACACCTCTTCTCGAGCTCTACGTAAAGCGTCAGGATGATGCTCGCGCATTTGGAG 103
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9 CAAAGCCTTGTCTCGAGTGTATGTGAAGCCTCAGGATGATGACAGCGACGATCGGTG 68
QY 104 CGATCTTTTCTGTCAGGAATCTCGATGGAGTTGTATGCTCTTTATGAGATTTGGAGTTG 163
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69 CATGCTTATTTTGCCAGAAATTTTGGATGGAATCTACGCTCTTTACGAAGTGGGCTGTG 128
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129 TCTGCTGTTGAGGTAAAGAACTGTGAATGTCAATTCGGAAGGATACAAAAGACATTTTCGG 188
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QY 404 CAAAGTAGAGTTCCGATAGGAGGAAAGAGGAGCCATCGAGATTCGAAGATCTCCAGCAC 463
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
549 TGATGCCACGCTTCTCATCCCTGCGCGTGTGCGGGAGGAGTGTCTCGCT 599

RESULT 6
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LOCUS SWOV3MCM45F09SK Onchocerca volvulus molting L3 larva cDNA
DEFINITION (SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCM45F09 5',
mRNA sequence.
ACCESSION BF400411 GI:11386455
VERSION BF400411.1
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
REFERENCE 1 (bases 1 to 671)
AUTHORS Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
JOURNAL Genes expressed in molting L3 larvae of Onchocerca volvulus
COMMENT Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomes@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1..671
/organism="Onchocerca volvulus"
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/mol_type="mRNA"
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/clone="SWOV3MCM45F09"
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/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3)"
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigman@nyc.org)."

ORIGIN
Query Match 24.0%; Score 209.4; DB 2; Length 671;
Best Local Similarity 75.5%; Pred. No. 8.3e-50;
Matches 274; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

QY 46 AAACCTCTTCTCGAGCTCTACGTAAAGCGTCAGGAATTTGATGCTCGCGCATTTGGAGCC 105
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157 TGCTTTGTTTGTCAAGAATTTTGGATGGAACTTTTACGCTCTTTATGAGATTTGGCGTTGT 216
QY 166 CGAGTCGAAGTGAAGACTGTCAAGTGAATTTCTGAAGCATTTTAAGAACTTTCTTCGGA 225
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 CGAGTTGAAGTGAAGACAGATAAATCATTAATTTCTGAAGCATTCAAAAGAGTTTCTTCGGA 276
QY 226 GCACAAACCCAGCTTATGATTTGAAGAGGAAAGAGCTGCATACACTGATAATCGAGAG 285
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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394 CCAGTGTAGAGAAACGAATTTGAAAGTTTGTACAGAAATTTCAAATCTTTTGGGATCC 453
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Db |||
454 AAA 456

RESULT 7
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LOCUS BE029008
DEFINITION kp23f02.v1 TBN95TM-SSFH Strongyloides stercoralis cDNA 5' similar
to WP.F26H11.5 CE15912 ;, mRNA sequence.
ACCESSION BE029008
VERSION BE029008.1
KEYWORDS EST.
SOURCE Strongyloides stercoralis
ORGANISM Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidae; Strongyloidea; Strongyloides.
REFERENCE 1 (bases 1 to 567)
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**AUTHORS** McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dance, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

**TITLE** The Washington Univ. Nematode EST Project, 1999

**JOURNAL** Unpublished (1999)

**COMMENT** Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: es@wustl.wustl.edu  
The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutman@nih.gov). DNA sequencing by: Washington University Genome Sequencing Center St. Louis.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 418.

**FEATURES** source  
1..567  
/organism="Strongyloides stercoralis"  
/mol\_type="mRNA"  
/strain="Filariform larvae obtained from humans"  
/db\_xref="taxon:6248"  
/lab\_host="XL-1 Blue MRF" (Stratagene)  
/clone\_lib="TBN957M-S5FH"  
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1: EcoRI; Site 2: XhoI; mRNA was purified from 4 x 10E5 filariform larvae which had been isolated from infected humans. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the EcoRI site to the XhoI site. The library has an amplified titer of 1.5 x 10E6 pfu/ml and an amplified, undiluted titer of 7 x 10E9 pfu/ml. The average insert size of the unamplified library is 975 bp (range, 500-1500)."

## ORIGIN

Query Match 23.3%; Score 203.6; DB 2; Length 567;  
Best Local Similarity 61.5%; Pred. NO. 3.9e-48;  
Matches 348; Conservative 0; Mismatches 209; Indels 9; Gaps 1;

QY 190 GTGATTTCTGAGCACTTTAAGAGAACTTTCTCGAGCACACACCGATTATGATGAA 249  
DB 1 GTTATTTCTGAGCTTTTAAAAATCTTTCTTGCGATCACTTCAATTTATGATGAA 60

QY 250 GAGGAAAAGAGCTGACATACACTGATATCGAGAGATTGAAGGACGATCTTTTCATTG 309  
DB 61 GCTTCCAAAGATGCAACATATTCAGATATAGAGATTTGAAGTAGAATATTTTCATCTT 120

QY 310 GCAAGGAATTCAGTTTCCACTTTTGAAGAGATCCATCCGCTGAGAGAGAAATAGAG 369  
DB 121 GCCAAGGAATTTGATGTGGCTCTTTTGAAGAAAGATATTACTGTTGAAGAGATTATTCAA 180

QY 370 AACTTGTACAGGAATCTCAAACTGTTCTCGAGCAAAAGTAGAGTTGCGATAAGGGAATA 429  
DB 181 TCACCTTATAGAAATTTAAATTTCTTAAAGCAAAACTGATCATGATAAGTTAG 240

QY 430 AAG-----GAGCCATCAGAGTTGAAGATCTTCCAGCACAGATTAAGTTCACTAC 480  
DB 241 AAGATAAATAAGAAATAATCTTCAAGAGAGTTTACCACAATCTGTTGTAGCTTGTGCGT 300

QY 481 AATCAGTCTGTGAGCACTACTCAATATTCATCTGATGCTATCCGAGAGAAATCTCGA 540  
DB 301 ACATAATTACTAGAACAAATTAGATCAATTCATTTGTTAGCAGAGGTTCAAGA 360

QY 541 TATCTACTTGAAACAGATGATGACTGAATATGACTGTGAACCTGATGCCACGCTTTCATCAT 600  
DB 361 TATTATTATCACAAAGTTTGTGTGAGTATGATTGTGAATTGATGCCAAGATTACATCAT 420

QY 601 ATTCGAATTATGATGTTGCTACTTCTTGGATTCATATTCACATAATTTTCACTCATCTC 660

DB 421 ATTAGAATTGTTGCTCAAGATTATTAGATTATGAAATTCACATAATGTTACCTATGTA 480  
QY 661 TGGGCTTATATCCCTCACTGATACCGTACAGCAGCATTTATTGAGAGTTGTCGCCGCGAT 720  
DB 481 TGGAAATTATATGCTTACTGCTATAGAGCTGTGCTGCTTCGATTGAAGTTGCCACGCTGAT 540  
QY 721 CAGGACATTTATTCATCACTATAAAGA 746  
DB 541 CAACATATTATACACCATACAGAGA 566

## RESULT 8

AI043403

LOCUS

DEFINITION

BSBmFMSZ06110SK Brugia malayi microfilaria cDNA (SAW941S-BmMf)

Brugia malayi cDNA clone BSBmFMSZ06110 5', mRNA sequence.

ACCESSION

AI043403

VERSION

AI043403.1 GI:32866660

KEYWORDS

EST.

SOURCE

Brugia malayi

ORGANISM

Brugia malayi

REFERENCE

1 (bases 1 to 483)

AUTHORS

Williams, S.A.

TITLE

Genes expressed in microfilaria of Brugia malayi

JOURNAL

Unpublished (1995)

COMMENT

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

EST submitted by Molecular Parasitology Group, New England Biolabs,

Inc., 32 Tozer Road, Beverly, MA, 01915, USA, Email:

dnaeq@neb.com. SZ in the clone designation, refers to 'Subtracted

Method Z'. The numerical designation after the SZ refers to the

microtiter tray number (01 - 48) followed by the letter and number

of the microtiter tray position. Method 'Z' refers to sequenced

clones which have been selected after hybridization subtraction

using highly redundant clones present in the gridded library

(18,000 mass-excised colonies gridded as a high density array on

nylon filters). Colonies not represented in the probe sets were

used as templates for the sequencing reactions.

Seq primer: pBluescript SK.

FEATURES

Location/Qualifiers

1..483

/organism="Brugia malayi"

/mol\_type="mRNA"

/strain="TRS Labs"

/db\_xref="taxon:6279"

/clone="BSBmFMSZ06110"

/lab\_host="XL1-Blue MRF"

/clone\_lib="Brugia malayi microfilaria cDNA

(SAW941S-BmMf)"

/note="Vector: lambda UniZap XR; Site 1: EcoR I; Site 2:

Xho I; Lymphatic filarial nematode parasite of humans.

mRNA was prepared from microfilariae of Brugia malayi

isolated from jirds and converted to double stranded cDNA

using reverse transcriptase and oligo(dT) followed by

RNase H and DNase I. The library had 3.5 x 10E5

independent recombinants and average insert size was 900

base pairs. The library was constructed by Lori Saunders.

The library is available from Dr. S.A. Williams, email

genome@smith.edu."

## ORIGIN

Query Match 23.1%; Score 202; DB 1; Length 483;  
Best Local Similarity 75.9%; Pred. NO. 1.1e-47;  
Matches 274; Conservative 0; Mismatches 83; Indels 4; Gaps 2;



45	AAAACTCTTCTCGAGCTTACGTAAAAGCGTCAAGAAATTGATGCTCGCGCAATTGGAGC	104
125	AAAAACGGCTTCTAGAGCTTTATGTTAAGGCCTCTGGAAATCGAAAAATCGTCGCAATGGTGC	184
105	CGATCTTTTCTCTCAGGAATTTCTGGATGGAGTTGTATGCTCTTTATGTAGAAATGGAGTTGC	164
185	ATGTTGTTGTTTGTCAAGAAATTTCTGGATGGAACTTTTACGCTCTCTATGAAATTTGGAGTTGT	244
165	ACGAGTTCGGAAGTGAAGACTGTCAACGTTAAATTTCTGAGCAATTTAAAGAAGAACTTTC	223
245	TCGAGTTGAAGTGAAGAAACAGTAAACATCAATTTCTGAAGCAATTTAAAGAGAGTTTCTTCGG	304
224	GAGCACAAACCCAGCTATTATGATTCGAAGAGGAAAAAGAGCTGACATACACTGATAATCGAG	283
305	GAGCACAAACCCAGCTATTATGTTGGGAAACAAGAATG---CAACTTATACTGCACATCTGTG	361
284	AGATTGAAGGACGGATCTTTTCATTTGGCAAGGAAATTCAAATGTTGCCACTCTTTGAAAAGG	343
362	AAATTGAGGACGCAATTTTCCATTTAGCAAAAGANTTCATGTGCCACTATTATTGAGAAAG	421
344	ATCCATTCGCGCTGAGAAGAGAAATAGAGAACTTTGTACAGGAACCTTCAAACCTGTTCTCTCGAG	403
422	ATCCAGTGGTNGAGAAACGAATCGAAAGTTTGTGNCAGAAACTTCCAAATCTTTTTCACGAT	481
404	C 404	
482	C 482	
Qy		
Db		

<b>RESULT</b>	9	.	.	.
CK242284				
<b>LOCUS</b>				
<b>DEFINITION</b>	CK242284	566 bp	mRNA	linear EST 11-DEC-2003
	rx08a04.y1 Meloidogyne paranaensis egg SMART pGEM Meloidogyne			
	paranaensis cDNA 5' similar to WP:CE25711 Y105E8E.Y ; mRNA			

```

The vector to vector length is 632
Seq primer: Sp6.
Location/Qualifiers
1. .566
/mol_type="mRNA"
/organism="Meloiodogyne paraensis"
/db_xref="taxon:189293"
/tissue_type="whole organism"
/dev_stage="egg"
/lab_host="DH10B"
/clone_lib="Meloiodogyne paraensis egg SMART pGEN"
/notes="Vector: pGEN-11zf(+). (Promega); Site 1: XhoI;
Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was
concentrated and purified using Dynabeads (Dynal) and mRNA
eluted for first strand synthesis. First strand cDNA was
created using MMV RT (Powerscript, Clontech) and primed
with oligo(dT) with XhoI site (primer CDS11f/3-XhoI) and
5' SMART 'anchor' added using chimeric DNA-RNA oligo
(SMART-NotI-r-GGG). 12 PCR cycles were done using first
strand and primers specific to SMART oligo(5' PCR-primer)
and 3' end(XhoI-No-dT). Double stranded cDNA was digested
using XhoI/NotI, fractioned on Chroma-spin 400 columns
(Clontech) and ligated to digested pGEN-11zf(+). plasmid.
Chemically competent DH10B cells were used as host cells.
Library constructed by Joanna Carlson."

```

ORIGIN	Query Match	21.6%	Score 189;	DB 7;	Length 566;
	Best Local Similarity	67.3%;	Pred. No. 7.4e-44;		
	Matches 267;	Conservative 0;	Mismatches 130;	Indels 0;	Gaps 0;
Qy	440	CGAGAGTTGAGATCTTCAGACAGATTAAGTTCACATCGAGTCTGTGAGCAAC	499		
Db	38	CAATAAGAGGGCCCTCCCCACAGGTGACATCTTCACACAATAATATTGGAGCAAT	97		
Qy	500	TATCCAATATTGATCAGTTGCTATCCGAGAGAAAATCTCGATATCTACTTGGAAACAGTA	559		
Db	98	TGGCCAATATTGACCAAGTTGTTGGCTGATCGTTCTCTCGTTATCTCTAAGTGAGTCAA	157		
Qy	560	TGACTGAATATGACTGTGAACTGATGCCAGGCTTTCATCATATTCGAATATTGGATGT	619		
Db	158	TGACTGAATATGACTGTGAGATTAATGCCAGTTTGACACCATATTCGTATCATTTGGAGAAC	217		
Qy	620	CACCTCTTGGATTCGATATTCCACATAATTTCACTCATCTCGGGCTTATATCTCACTG	679		
Db	218	GCCTTTTGAATTTTACATTCACAGTCAATTCATCATTTACGGCATATATTAACTG	277		
Qy	680	CATACCGTACAGCAGCATTTATTGAGAGTTGTCCCGCGGATCAGGACATTTATCATCACT	739		
Db	278	CATATCGAACAGCTGGGCTTTATTGAATCTTGTCCGGCTGATCAAGATAATTTTGCATCATTT	337		
Qy	740	ATAAAGAACAAATGAATCTGTTCCACAAAATCAACGTGAAACCCCTCCAATGCCCAACAAAA	799		
Db	338	ATAAGGAACAAATTAACATTTGGCAATTTGATATGCGAGTGACATTTGAAGCACCAACAAAGA	397		
Qy	800	CGCACAAATTCGGAAAAAGTGCTATCGGATATTCG	836		
Db	398	CATTAAACCATTCAGAAAGATGTCTTCAAGATATACG	434		

RESULT 10	CB374401	480 bp	linear	EST 18-MAR-2003
LOCUS	CB374401			
DEFINITION	ru99h02.y1 Heterodera glycines virgin female Heterodera glycines cDNA 5' similar to WP:CE25703 Y1058C.A ;, mRNA sequence.			
ACCESSION	CB374401			
VERSION	CB374401.1	GI:29049758		
KEYWORDS	EST.			
SOURCE	Heterodera glycines			
ORGANISM	Heterodera glycines			
	Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodidae; Heteroderinae; Heterodera.			
REFERENCE	1 (bases 1 to 480)			



QY 508 ATTGATCAGTTGCTATCCGAGAGAAAACTCGATATCTACTTGGAAAAAGAGTATGACTGAA 567  
 |||||  
 Db 67 ATTGACAAATTGTTAGCAAAAGAGGTTCAAGATATTGTTATCACAAAGTTTATGTGA 126  
 |||||  
 QY 568 TATGACTGTGAAGTATGACGCTCTTCAATATATCGAATATTGGATGTGCACTTCTT 627  
 |||||  
 Db 127 TATGATTTGTGAGTTAATGCAAGATTACATCATATTTCGAATTTGTTGGTCAAAAGATTATTA 186  
 |||||  
 QY 628 GGATTCGATATTCCACATAATTTCACTCATCTCTGGCTTATATCTCACTGCATACCGT 687  
 |||||  
 Db 187 GATTTTGAATTTCCACATAATTTTACTTATTTATGGAATTAATTCTTACTGCCCTATAGA 246  
 |||||  
 QY 688 ACAGCAGCATTTTATTGAGAGTTGTCCCGCGCATGACGAGCAATTTATCATCACTATAAGAA 747  
 |||||  
 Db 247 ACAGCTGCTTTTATTGAAAGTTGCCGAGCTGATCAAGATATCTTACACCATTTATAAGAA 306  
 |||||  
 QY 748 CAAATGAATCTGTTCAAAATCAAGTGAAACCTCCATGCCAACAAAACGACACACA 807  
 |||||  
 Db 307 CAAATTAATATTTTACCATCAAGCTGAACATTTACAGCACCAACAAAATCACACA 366  
 |||||  
 QY 808 ATTCCGAAAAAGTCTATCGGATAT 833  
 |||||  
 Db 367 ATTCCAAAGGCGGTGTTAGTGAAT 392  
 |||||

RESULT 12  
 LOCUS CK349229 450 bp mRNA linear EST 22-DEC-2003  
 DEFINITION hgghai008 Gland Cell LD PCR cDNA Library Heterodera glycines  
 cDNA, mRNA sequence.

ACCESSION CK349229  
 VERSION CK349229.1 GI:40304842

KEYWORDS EST

SOURCE Heterodera glycines

ORGANISM Heterodera glycines

REFERENCE 1 (bases 1 to 450)  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

AUTHORS Gao, B., Allen, R., Maier, T., Davis, E.L., Baum, T.J. and Hussein, R.S.  
 TITLE Identification of putative parasitic genes expressed in the  
 esophageal gland cells of the soybean cyst nematode, Heterodera  
 glycines

JOURNAL Mol. Plant Microbe Interact. 14 (10), 1247-1254 (2001)

COMMENT Contact: Tom Maier  
 Department of Plant Pathology, Baum Lab  
 Iowa State University  
 351 Bessey Hall, Ames, IA 50011, USA  
 Tel: 515-294-8854  
 Fax: 515-294-9420  
 Email: tmaier@iastate.edu  
 Heterodera glycines Gland Cell LD PCR cDNA Library, single pass  
 sequence.

FEATURES Location/Qualifiers

1..450  
 /organism="Heterodera glycines"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:51029"  
 /cell\_type="gland"  
 /dev\_stage="mixed parasitic juvenile"  
 /clone\_lib="Gland Cell LD PCR cDNA Library"  
 /note="Organ: gland cell; Vector: pGEM-T Easy"

ORIGIN

Query Match 19.5%; Score 170.2; DB 7; Length 450;  
 Best Local Similarity 65.9%; Pred. No. 2.2e-38;  
 Matches 247; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 44 CAAACCTCTTCTCGAGCTCTACGTAAAGCGTCAGGAATTCATGTCGCCGATTTGGAG 103  
 |||||

Db 58 CAAAGCCTTTGTCGAGTTGTATGTAAGGCTTCAGGGATTACAGCCGACCATCGGTG 117  
 |||||

QY 104 CCGATCTTTTCTGTGAGGAATTCGGATGGAGTTGTATGCTCTTTATGAGATGGAGTTG 163  
 |||||

Db 118 CATGCTTATTTTCCCAAGAAATTTTGGATGGAACCTACGGCTCTTACGAAGTGGGCTG 177  
 |||||  
 QY 164 CACGAGTCGAAGTGAAGACTGTCAACGTGAATTCCTGAAGCATTTTGAAGAGACTTTCTCG 223  
 |||||  
 Db 178 TTCGTGTTGAGGTAAAACTGTGAATGTCGATTCGGAAGGATACAAAAGCACTTTTCGG 237  
 |||||  
 QY 224 GAGCAACACCCAGCATTTATGATTGAAGAGGAAAAAGAGCTGACATACACTGATAATCGAG 283  
 |||||  
 Db 238 GAGCACGCCCAATTAATGTTGGAACAAGACAAAGGACCGCAATTCGGGACACACTG 297  
 |||||  
 QY 284 AGATTGAAGGACGATCTTTTCAATTTGGCAAGGAATTCAAATGTTCCACTCTTTTGAAGAG 343  
 |||||  
 Db 298 ACATCGAGCGACGATTTTCCAACTTTTCCAACTTTTCCAACTTTTCCAACTTTTCCAACT 357  
 |||||  
 QY 344 ATCCATCGCTGAGAGAGATAGAGAACTTGTACAGGAACCTTCAAACTGTTTCTCGCGAG 403  
 |||||  
 Db 358 ATCCGGAAGTGGCAAGACCATCCAGGATTTGTACAGGAACCTTCAAAATATTCTCCAAG 417  
 |||||  
 QY 404 CAAAGTAGAGTTTCG 418  
 |||||  
 Db 418 CCAAAACGAATTTTG 432  
 |||||

RESULT 13

LOCUS CA868923

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..567

/organism="Haemonchus contortus"

/mol\_type="mRNA"

/db\_xref="taxon:6289"

/lab\_host="DH10B"

/clone\_lib="Haemonchus contortus intestine pAMP1 v1"

/note="Vector: pAMP1; Site 1: NotI; Site 2: SalI; The

library was constructed by Claire Murphy and Dr. James

McCarter at Washington University, St. Louis. The cDNA was

made by using Dynabead oligo-dT priming (Dynal). PCR based

High quality sequence stop: 410.

Location/Qualifiers

1..567

/organism="Haemonchus contortus"

/mol\_type="mRNA"

/db\_xref="taxon:6289"

/lab\_host="DH10B"

/clone\_lib="Haemonchus contortus intestine pAMP1 v1"

/note="Vector: pAMP1; Site 1: NotI; Site 2: SalI; The

library was constructed by Claire Murphy and Dr. James

McCarter at Washington University, St. Louis. The cDNA was

made by using Dynabead oligo-dT priming (Dynal). PCR based

High quality sequence stop: 410.

Location/Qualifiers

1..567

/organism="Haemonchus contortus"

/mol\_type="mRNA"

/db\_xref="taxon:6289"

/lab\_host="DH10B"

/clone\_lib="Haemonchus contortus intestine pAMP1 v1"

/note="Vector: pAMP1; Site 1: NotI; Site 2: SalI; The

library was constructed by Claire Murphy and Dr. James

McCarter at Washington University, St. Louis. The cDNA was

made by using Dynabead oligo-dT priming (Dynal). PCR based

High quality sequence stop: 410.

Location/Qualifiers

1..567

/organism="Haemonchus contortus"

/mol\_type="mRNA"

/db\_xref="taxon:6289"

/lab\_host="DH10B"

/clone\_lib="Haemonchus contortus intestine pAMP1 v1"

library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pMPL. Intestinal RNA was provided by Dr. Douglas Jassmer of Washington State University (djaemer@vetmed.wsu.edu)."

```

ORIGIN
Query Match      17.5%; Score 152.6; DB 6; Length 567;
Best Local Similarity 69.8%; Pred. No. 3.4e-33;
Matches 206; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 559 ATGACTGAATATGACTGTGAATGATGCCACGCTTTCATCATATTCGAATTAATGATTG 618
    |||||
Db 4 ATGACGGAATATGATTGTGAATTAATGATGCCACGCTTTCATCATATTCGAATTAATGATTG 618
    |||||
QY 619 TCATCTCTTGGAATTCATATTCACATATTCATCTCTGCGCTTATATCTCATCT 678
    |||||
Db 64 AGAATGCTCAATTTGCAATTCCTCGCAATTTAACTTCTGTGGAATTAACGCTACTGACC 123
    |||||
QY 679 GCATACCGTACAGCAGCATTTATTGAGAGTGTCCGCGGATCAGACATATTCATCAC 738
    |||||
Db 124 GCTATCGAACGCGCTTCTATTGAGAGCTGTCCGCGGATCAGACATATTCATCAT 183
    |||||
QY 739 TATAAGAACAAATGAATCTGTTCAAAATCAACGTGAACCTCCAAATCGCCAAACAAA 798
    |||||
Db 184 TATAAGGACAACTAAATATGTTCAAAATCAGCGTGAGACGTACAGTCCGCGACGAAG 243
    |||||
QY 799 ACGCACACATTCGCGGAAAAGTGCTATCGGATATTCGTTTAAAGGACTTGCTC 853
    |||||
Db 244 ACACATACCATTCGCGAAGAGGTGTGATGGACATCAGAAGAAGTGGGCTGGATC 298
    |||||

```

```

RESULT 14
BG225023      426 bp mRNA linear EST 09-MAY-2001
LOCUS      kp61c08.y1 TN95TM-SSFH Strongyloides stercoralis cDNA 5' similar
DEFINITION to SW:CL12 HUMAN O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 ;,
            mRNA sequence.
ACCESSION      BG225023
VERSION      BG225023.1 GI:12712578
KEYWORDS      Strongyloides stercoralis
SOURCE      Strongyloides stercoralis
ORGANISM      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Panagrolaimoidea; Strongyloidea; Strongyloides.
REFERENCE      1 (bases 1 to 426)
AUTHORS      McGarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
            Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
            Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
            Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
            Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
            Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
            McCann, R., Waterston, R. and Wilson, R.
            The Washington Univ. Nematode EST Project, 1999
            Unpublished (1999)
            Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Dr. Thomas Nutman and colleagues of
            NIAID, NIH (nutman@nih.gov). DNA Sequencing by: Washington
            University Genome Sequencing Center St. Louis.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 418.
            Location/Qualifiers
            1..426
            /organism="Strongyloides stercoralis"
            /mol_type="mRNA"
            /strain="Filariform larvae obtained from humans"
            /db_xref="taxon:6248"

```

## FEATURES

source

/lab\_host="XL-1 Blue MRF" (Stratagene)"

/clone\_lib="TEN95TM-SSFH"

/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1:

EcoRI; Site 2: XhoI; mRNA was purified from 4 x 10<sup>8</sup>5

filariform larvae which had been isolated from infected

humans. cDNA was constructed and, using adaptors, was

cloned unidirectionally into the vector from the EcoRI

site to the XhoI site. The library has an unamplified

titer of 1.5 x 10<sup>6</sup> pfu/ml and an amplified, undiluted

titer of 7 x 10<sup>9</sup> pfu/ml. The average insert size of the

unamplified library is 975 bp (range, 500-1500)."

## ORIGIN

```

Query Match      16.8%; Score 146.8; DB 4; Length 426;
Best Local Similarity 70.5%; Pred. No. 1.6e-31;
Matches 196; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 575 GTGAACGATGCCACGCTTTCATCATATTCGAATTAATGATTGCTCACTTCTTGATTTCG 634
    |||||
Db 1 GTGAATGATGCCAAGATTACATCATATTAAGATTGTGTCAAAGATTATTAGATTTCG 60
    |||||
QY 635 ATATTCCACATAATTTTCACTCATCTCTGGGCTTATATCTCACTGCATACCGTACAGCAG 694
    |||||
Db 61 AAATTCCACATAATTTTACCTTATTATGGAATTATATTTCTACTGCTATAGAACTGCTG 120
    |||||
QY 695 CATTATTGAGAGTGTCCGCGGATCAGACATTAATCATCTATATAAGAAATTAATAGATTTCG 754
    |||||
Db 121 CTTTCATGGAAGTTGCCAGCTGATCAAGATATTTTACACCATTTACAGGAAACAATTA 180
    |||||
QY 755 ATCTGTTTCAAAATCAACGTGAACCTCCAAATCGCCAAACAAACCAACCAATTCACAAATTCCTG 814
    |||||
Db 181 ATATTTTCAAAATCAACGTGAACCTCCAAATCGCCAAACCAACCAATTCACAAATTCCTG 240
    |||||
QY 815 AAAAAGTGTATCGGATTAATTCGTTTAAAGGACTTGCT 852
    |||||
Db 241 AGGCAGTGTATGAAATAAGCGGATTAAGAACTTGAAT 278
    |||||

```

## RESULT 15

```

CV508408      324 bp mRNA linear EST 05-OCT-2004
LOCUS      kc71g05.y1 Xiphinema index CSEQL01 Xiphinema index cDNA 5' similar
DEFINITION to WP:CE25711 Y105B8E.Y ;, mRNA sequence.
ACCESSION      CV508408
VERSION      CV508408.1 GI:53806521
KEYWORDS      EST.
SOURCE      Xiphinema index
ORGANISM      Eukaryota; Metazoa; Nematoda; Enopleia; Dorylaimida; Dorylaimina;
            Longidoroidea; Longidoridae; Xiphinema.
REFERENCE      1 (bases 1 to 324)
AUTHORS      McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
            Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
            Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
            Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
            Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
            Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
            McCann, R., Waterston, R. and Wilson, R.
            The Washington Univ. Nematode EST Project, 1999
            Unpublished (1999)
            Contact: Mitreva M
            The Washington Univ. Nematode EST Project, 2004
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library materials provided by: J.T. Jones Library constructed by:
            Incyte Genomics (for J.T. Jones)
            Putative full length read
            The vector to vector length is 325
            Seq primer: -21UPPOT primer.
            Location/Qualifiers

```

## FEATURES

```
source
1..324
/organism="Xiphinema index"
/mol_type="mRNA"
/db_xref="taxon:46003"
/sex="mixed"
/dev_stages="mixed"
/lab_host="GC10 (only ligation mix supplied)"
/clone_lib="Xiphinema index CSEQDL01"
/notes="Vector: pBluescript SK+; Site 1: 5'; NotI; Site 2:
3': EcoRI; The library was made from mRNA isolated from
total RNA using oligo dt cellulose. Total RNA was
generated from mixed stage X. index extracted from soil
around fig (Ficus carica) roots. Nematodes were cleaned by
passing through a series of sieves. Pure X. index were
obtained by hand sorting of nematodes. The library was
constructed by Incyte Genomics by cloning cDNA
directionally into in the pBluescript (SK+) vector using
NotI and EcoRI sites. The library was provided by John T.
Jones (jjones@scri.sari.ac.uk) at SCRI, Nematology
Department. Sequencing by: Washington University Genome
Sequencing Center, St. Louis, MO."

ORIGIN
Query Match      15.9%; Score 138.6; DB 7; Length 324;
Best Local Similarity 66.7%; Pred. No. 3.6e-29;
Matches 198; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 536 CTCGATATCTACTTGGAAACAGTATGACTGATATGACTGTGAACGTGATGCCACGTCTTC 595
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 26  CACGTTATCTTTTGGGTTGGTCCATGACGGAATACGATTCGATTCGATTCGCCCCCTGC 85

QY 596 ATCATATTGGAATTATTGGATTGTCACTTTTGGATTGATATCCACATAATTTCACTC 655
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86  ATCATATTGGAATCGCGGTTCAAAATTATGCGGTGTGAAATCCACACATCTGGTTT 145

QY 656 ATCTCTGGCTTATATCTCACTGATACCGTACAGCAGCATTTATTGAGAGTTGTCCCG 715
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 ATTTGTGGAATTATATGCTGACGAGTATCGAACTGCCGCAATTTATCGAGTCGTGCCCGG 205

QY 716 CCGATCAGGACATTATTTCATCACTATAAGAACAAATGAATCTGTTCAAAATCAACGTG 775
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 CTGATCAAGACATCATTTTCCATTACAAGAACAAATTTGAACATTCCTCCCTGGACACGCG 265

QY 776 AAACCCCTCCAATCGCCAAACAAAACGACACAAATTCGGAAAAAGTGTATCGGATA 832
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 AAAGTCTTCAATTGCCTACAAAACGCATACGATTCGCCGAGATGCTCTTGGCCGAAA 322
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Search completed: March 10, 2005, 02:20:41  
Job time : 3566 secs

use rouge blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 23:54:49 Search time 194 Seconds  
(without alignments)  
7363.245 Million cell updates/sec

Title: US-10-612-379-1  
Perfect score: 873  
Sequence: 1 atggcagaagcttaccagat.....ccgagttaatttcattaa 873

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA:  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	76.4	8.8	1090	US-09-270-767-26167	Sequence 26167, A
2	76.4	8.8	1880	US-09-270-767-10712	Sequence 10712, A
c 3	47.4	5.4	7218	US-08-232-463-14	Sequence 14, Appl
4	46.4	5.3	819	US-08-792-014-2	Sequence 2, Appl
5	46.4	5.3	819	US-09-443-948-2	Sequence 2, Appl
6	46.4	5.3	819	US-09-690-196-2	Sequence 2, Appl
7	43.4	5.0	1652	US-09-620-312D-815	Sequence 815, Appl
8	43.4	5.0	1689	US-09-949-016-5780	Sequence 5780, Appl
9	41	4.7	1068	US-09-710-794-3	Sequence 3, Appl
10	39.8	4.6	601	US-09-949-016-107953	Sequence 107953, A
11	39.8	4.6	601	US-09-949-016-107954	Sequence 107954, A
12	39.8	4.6	390890	US-09-949-016-14720	Sequence 14720, A
c 13	38.2	4.5	1529	US-09-533-029-49	Sequence 49, Appl
14	38.4	4.4	1141	US-09-808-708B-22	Sequence 22, Appl
15	38.4	4.4	253345	US-09-949-016-12656	Sequence 12656, A
16	38.4	4.4	253364	US-09-949-016-13639	Sequence 13639, A
17	37.8	4.3	832	US-09-621-976-2813	Sequence 2813, Appl
c 18	37	4.2	14066	US-09-601-198-56	Sequence 56, Appl
19	36.8	4.2	1664976	US-08-916-421B-1	Sequence 1, Appl
c 20	36.8	4.2	1664976	US-09-692-570-1	Sequence 1, Appl
21	36	4.1	42381	US-09-949-016-12012	Sequence 12012, A
22	36	4.1	168394	US-09-949-016-13002	Sequence 13002, A
23	36	4.1	183770	US-09-949-016-15494	Sequence 15494, A
24	35.8	4.1	95561	US-09-949-016-12768	Sequence 12768, A
25	35.8	4.1	95561	US-09-949-016-13306	Sequence 13306, A
26	35.8	4.1	95561	US-09-949-016-13307	Sequence 13307, A
c 27	35.6	4.1	601	US-09-949-016-86515	Sequence 86515, A

28	35.6	4.1	61462	4	US-09-949-016-17522	Sequence 17522, A
c 29	35.6	4.1	183112	4	US-09-949-016-14184	Sequence 14184, A
30	35.4	4.1	601	4	US-09-949-016-141596	Sequence 141596, A
c 31	35.4	4.1	832	4	US-09-621-976-2813	Sequence 2813, Appl
32	35.4	4.1	236964	4	US-09-949-016-15753	Sequence 15753, A
c 33	35.4	4.1	250715	4	US-09-949-016-13294	Sequence 13294, A
c 34	35	4.0	601	4	US-09-949-016-141597	Sequence 141597, A
35	35	4.0	1497	3	US-09-232-468A-17	Sequence 17, Appl
36	35	4.0	1497	4	US-09-784-984B-14	Sequence 14, Appl
37	34.6	4.0	696	4	US-09-583-110-1334	Sequence 1334, Appl
38	34.6	4.0	789	4	US-09-107-433-176	Sequence 176, Appl
39	34.6	4.0	921	4	US-09-270-767-8688	Sequence 8688, Appl
40	34.6	4.0	921	4	US-09-270-767-23970	Sequence 23970, A
41	34.2	3.9	1086	4	US-09-248-796A-59	Sequence 59, Appl
42	34.2	3.9	2082	4	US-09-248-796A-2564	Sequence 2564, Appl
c 43	34.2	3.9	343352	4	US-09-949-016-13498	Sequence 13498, A
44	34	3.9	55806	4	US-09-949-016-15605	Sequence 15605, A
45	33.8	3.9	601	4	US-09-949-016-37936	Sequence 37936, A

ALIGNMENTS

RESULT 1  
US-09-270-767-26167  
; Sequence 26167, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26167  
; LENGTH: 1090  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-26167

Query Match	8.8%;	Score 76.4;	DB 4;	Length 1090;
Best Local Similarity	52.5%;	Pred. No. 9.2e-14;		
Matches 167;	Conservative 0;	Mismatches 151;	Indels 0;	Gaps 0;
Qy	495	GCAACTATCCAATATTGATCAGTTGCTATCCGAGAGAAATCTCGATATCTTCTACTTGGAAA	554	
Db	28	GCATCTGGCGAAGATCAACGATCATCTGTCCGCGGCAACACGGCTTCTCTCACCGCGGA	87	
Qy	555	CAGTATGACTGAATATGACTGTGAACACTGATGCCACGCTTTCATCATATTCGAAATTTATGG	614	
Db	88	CACCATGTGCTGCTTCGACTGTGAGCTGATGCGCGGCTGCAGCACATCCGTGTGGCGGG	147	
Qy	615	ATTGTGACTTCTTGGATTGATATTCACATAATTTCACTCATCTCTGGGCTTATATCTT	674	
Db	148	CAAGTACTTTGTTCGACTTTGAAATCCGACGCACTTGCACGCCCTGTGGCGCTACATGTA	207	
Qy	675	CACGTGATACCGTACAGCAGCATTTATTGAGAGTTGTCCGCGCGATCAGACATTTATCA	734	
Db	208	TCACATGTACAGCTGGACGCGCTTCACACATCTGTCGCCGCGCCAGGACATTATCAA	267	
Qy	735	TCACATATAAGAAACAAATGAATCTGTTTCACAAATCAACGTGAAACCCCTCCAAATCGCCAAC	794	
Db	268	TCACTACAGCTGCACAGAGTCTCAAAATGAAGAGCAGGAGCTGGAGAGCTGGAGAGCCAC	327	
Qy	795	AAAAACGCACAAATTC	812	
Db	328	GTTTACCACATATTC	345	
RESULT 2				
US-09-270-767-10712				
; Sequence 10712, Application US/09270767				

Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10712  
LENGTH: 1880  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-10712

Query Match 8.8%; Score 76.4; DB 4; Length 1880;  
Best Local Similarity 52.5%; Pred. No. 1.3e-13;  
Matches 167; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 495 GCAACTATCCATATATGATCACTGCTATCCGAGAGAAAATCTCGATATCTACTTGGAAA 554  
DB 818 GCATCTGCGCAAGATCAACGATCATCTGTCCGCGCAACACGCGCTTCTCACCGCGGA 877  
QY 555 CAGTATGACTGAATATGACTGTGAATGATGCACTCTTCAATCATATTCGAATTTATTGG 614  
DB 878 CACCATGTGCTCTCGACTGTGAGCTGATGCGCGCGCTGAGACATCCGTGTGGCGGG 937  
QY 615 ATGTGACTCTTGTGATTCGATATTCACATTAATTTCACTATCTCTGGGCTTATATCCT 674  
DB 938 CAACTACTTTGTGCACTTTGAAATCCGACGACTTGAACGCGCTGTGGCGCTACATGTA 997  
QY 675 CACTGCATACCGTACAGCAGCATTTATTGAGAGTTGTCGCCCGATCAGGACATTTCA 734  
DB 998 TCATATGACAGCTGGAGCGCTTACACATCTGTGCGCGCGCGACGAGCATTTATCAA 1057  
QY 735 TCATATTAAGAACAAATGAATCTCTTCAAAATCAAGTGAAGCCCTCCCAATCGCCAAAC 794  
DB 1058 TCATACAGAGCTGCAACAGAGTCTCAAAATGAGAGACAGGAGCTGGAGACGCCAC 1117  
QY 795 AAAACGACACAAATTC 812  
DB 1118 GTTACCACATACATTC 1135

RESULT 3  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fls  
US-08-232-463-14

Query Match 5.4%; Score 47.4; DB 1; Length 7218;  
Best Local Similarity 7.4%; Pred. No. 0.00047;  
Matches 27; Conservative 187; Mismatches 153; Indels 0; Gaps 0;

QY 86 ATGCTCCCGCATTTGGAGCCGATCTTTCTCTGTCAGGAATCTCGATCGAGTTGTATGCTC 145  
DB 1497 ATGTAGGCATCACGTAAATACCTATCTATGCAAGTAGTTAAAGAGATAGAAGAAATTTGG 1438  
QY 146 TTTATGAGATTGGAGTTGTCAGAGTCGAAGTGAAGACTGTCACGCTGAATTTCTGAAGCAT 205  
DB 1437 TACRR 1378  
QY 206 TTAAGAAGACTTTCTCGAGACACACCGATGATGATGATGATGATGATGATGATGATGATG 265  
DB 1377 RRR 1318  
QY 266 CATACACTGATATCGAGAGATGGAAGACGAGCTTTTCATTTTGGCAAGAAATTCATG 325  
DB 1317 RRR 1258  
QY 326 TTCACACTTTTGAAGAGGATCCATCCGCTCGAGAGAGAGATAGAGAACTTTGACAGAACT 385  
DB 1257 RRR 1198  
QY 386 TCAAACTGTTCTCGAGACAAAAGTAGAGTTGATAAGGAGAAAAGAGCCATCGAGAG 445  
DB 1197 RRR 1138  
QY 446 TTGAAGA 452  
DB 1137 RRRRRR 1131

RESULT 4  
US-08-792-014-2  
Sequence 2, Application US/08792014  
Patent No. 6063594  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN ANION CHANNEL  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS



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; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,014
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; US-08-792-014-2

Query Match          5.3%; Score 46.4; DB 3; Length 819;
Best Local Similarity 50.0%; Pred. No. 0.00029;
Matches 116; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 540 ATATCTACTTGGAAACAGTATGACTGGAATATGACTGTGCACTGATGCGACGCTCTTCATCA 599
DB 546 ATTTCTGATGCGCAATGAAATGACATTAGCTGATGCAACCTGCTGCCAACTGCATAT 605
QY 600 TATTCGAATTATTGGATTGTCACTTCTTGGATTTCGATATTCACATATTTTCATCATCT 659
DB 606 TGTCAGGTGGTGGCCAAAATAATCGCAACTTTTGATATTTCAAAGAAATGACTGGCAT 665
QY 660 CTGGCTTTATTCCTCACTGATACCGTACAGCAGCATTTTATGAGAGTTCGCCGCCGA 719
DB 666 CTGGAGATACCTAACTAATGATACAGTAGGAGCGGGTTACCAATACCTGTCCAGTGA 725
QY 720 TCAGGACATTATTCATCACTATAAGAACAAATGAATCTGTTCAAAATCAA 771
DB 726 TAAGGAGTTGAAATAGCATATAGTAGTGTAGCCAAAGAGACTCACCAGTAA 777

RESULT 5
US-09-443-948-2
; Sequence 2, Application US/09443948
; Patent No. 6228616
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN ANION CHANNEL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/443,948
; FILING DATE: 19-No. 6228616-1999
; CLASSIFICATION: <Unknown>

; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,014
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; US-09-443-948-2

Query Match          5.3%; Score 46.4; DB 3; Length 819;
Best Local Similarity 50.0%; Pred. No. 0.00029;
Matches 116; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 540 ATATCTACTTGGAAACAGTATGACTGGAATATGACTGTGCACTGATGCGACGCTCTTCATCA 599
DB 546 ATTTCTGATGCGCAATGAAATGACATTAGCTGATGCAACCTGCTGCCAACTGCATAT 605
QY 600 TATTCGAATTATTGGATTGTCACTTCTTGGATTTCGATATTCACATATTTTCATCATCT 659
DB 606 TGTCAGGTGGTGGCCAAAATAATCGCAACTTTTGATATTTCAAAGAAATGACTGGCAT 665
QY 660 CTGGCTTTATTCCTCACTGATACCGTACAGCAGCATTTTATGAGAGTTCGCCGCCGA 719
DB 666 CTGGAGATACCTAACTAATGATACAGTAGGAGCGGGTTACCAATACCTGTCCAGTGA 725
QY 720 TCAGGACATTATTCATCACTATAAGAACAAATGAATCTGTTCAAAATCAA 771
DB 726 TAAGGAGTTGAAATAGCATATAGTAGTGTAGCCAAAGAGACTCACCAGTAA 777

RESULT 6
US-09-690-196-2
; Sequence 2, Application US/09690196
; Patent No. 6503733
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN ANION CHANNEL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/690,196
; FILING DATE: 16-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/792,014
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0206 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-690-196-2

Query Match      5.3%; Score 46.4; DB 4; Length 819;
Best Local Similarity 50.0%; Pred. No. 0.00029;
Matches 116; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 540 ATATCTACTTGAACACGATGACTGATATGACCTGTAACCTGATGACCTGCTGCAACGCTTTCATCA 599
Db 546 ATTCTGATGCAATGAATGACATAGCTGATGACCTGCTGCAACGCTTTCATCA 605

Qy 600 TATTCGAATATTGGAATTGTCACTTCTTTGGATTGATATCCACATAATTTCACTCATCT 659
Db 606 TGTCAGGTGGTGGCAAAAATATCGCAACTTTGATATTTCAAAGAAATGACTGGCAT 665

Qy 660 CTGGCTTATATCTCACTGATACCTGATACCTGATACCTGATACCTGATACCTGATACCTGATACCT 719
Db 666 CTGGAGATACCTAATGATGATACCTGATACCTGATACCTGATACCTGATACCTGATACCTGATACCT 725

Qy 720 TCAGACATATTTCATCACTATAAGAAACAATGATCTGTTCAAAATCAA 771
Db 726 TAAGAGGTTGAATAGCATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777

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RESULT 7

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US-09-620-312D-815
; Sequence 815, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Fang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784C1P2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0

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; SEQ ID NO 815
; LENGTH: 1652
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (232)..(975)
US-09-620-312D-815

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Query Match      5.0%; Score 43.4; DB 4; Length 1652;
Best Local Similarity 52.5%; Pred. No. 0.0038;
Matches 95; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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Qy 549 TGGAAACAGTATGACTGATGATGACTGATGACTGATGACTGATGACTGATGACTGATGACTGATGACT 608
Db 756 TGGGACCAGCTAACACTGGCTGATTTGTTACCCCAAGCTGAACATTATTAAAGT 815

Qy 609 TATTGGATTGTCACTTCTTGATTCGATATTCCACATAATTTCACTCATCTCTGGGCTTA 668
Db 816 TGCTGCCAAGAAATATCGTACCTTTGACATTCAGCAGAAATTCAGAGAGTCTGGCGTTA 875

Qy 669 TATCCTCACTGCATACCGTACAGCAGCAATTTATTGAGAGTTGTCCCGCCGATCAGGACAT 728
Db 876 TCTCCACAATGCCCTATGCCCGTGAAGAATTTACCCACACGCTGCTCTGAAGACAAAGAAAT 935

Qy 729 T 729
Db 936 T 936

```

RESULT 8

```

US-09-949-016-5780
; Sequence 5780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5780
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5780

```

```

Query Match      5.0%; Score 43.4; DB 4; Length 1689;
Best Local Similarity 52.5%; Pred. No. 0.0039;
Matches 95; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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Qy 549 TGGAAACAGTATGACTGATGATGACTGATGATGACTGATGACTGATGACTGATGACTGATGACT 608
Db 746 TGGGACCAGCTAACACTGGCTGATTTGTTACCCCAAGCTGAACATTATTAAAGT 805

Qy 609 TATTGGATTGTCACTTCTTGATTCGATATTCACATAATTTCACTCATCTCTGGGCTTA 668
Db 806 TGCTGCCAAGAAATATCGTACCTTTGACATTCAGCAGAAATTTCTCAGAGTCTGGCGTTA 865

Qy 669 TATCCTCACTGCATACCGTACAGCAGCAATTTATTGAGAGTTGTCCCGCCGATCAGGACAT 728
Db 866 TCTCCACAATGCCCTATGCCCGTGAAGAATTTACCCACACGCTGCTCTGAAGACAAAGAAAT 925

Qy 729 T 729

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[illegible]

```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14720
; LENGTH: 390890
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(390890)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14720

```

```

Query Match      4.6%; Score 39.8; DB 4; Length 390890;
Best Local Similarity 52.0%; Pred. No. 1.2;
Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 324 TGTTCCACTCTTTGAAAGGATCCATCCGCTGAGAGAGAGATAGAGAACTTTGTACAGGAA 383
Db 314235 TGTAACACTCTGGGAAAGTAACTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314176

Qy 384 CTTCAAACTGTTCTCGAGCAAAAGTAGAGTTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 443
Db 314175 ATACTCTATGTTCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314116

Qy 444 AGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494
Db 314115 AGTTTAATACTTCCAGTCCACATATATGATGTTTCCATCTGTGCTTTGA 314065

```

```

RESULT 13
US-09-533-029-49
; Sequence 49, Application US/095333029
; Patent No. 666446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1529
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G553
US-09-533-029-49

```

```

Query Match      4.5%; Score 39.2; DB 4; Length 1529;
Best Local Similarity 58.6%; Pred. No. 0.08;
Matches 68; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 150 TGAGATTGGAGTTGCACAGTCGAGAGTGAAGACTGTCAACGTGAATTTCTGAAGCATTTAA 209
Db 249 TGAGGTTGATGCTAGACAGAGAGAGATGATAACAATAGAGTGAATTTCTGCTGTA 308

Qy 210 GAAGAACTTTCTCGAGCACAAACCCAGGATTTATGATTGAAGAGGAGGAGGAGGAGGAGGAG 265
Db 309 TAATAACTCTCTTGAAGCAGAACCGTCGAGTAATGATCAGGACGAGGAGGAGGAGGAGGAG 364

RESULT 14
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; NAME/KEY: promoter
; LOCATION: (1)...(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

```

```

Query Match      4.4%; Score 38.4; DB 4; Length 1141;
Best Local Similarity 8.5%; Pred. No. 0.12;
Matches 36; Conservative 183; Mismatches 207; Indels 0; Gaps 0;

Qy 284 AGATTGAAGGAGGAGATCTTTCATTTGCGAAAGGAAATCAATGTTCCTCTTTGAAAGG 343
Db 176 DDDTKYHMMNNNGCBTVMVRYKTRDWSBKRMNYGMBWKNWSYDYVYVWVWDDMCK 235

Qy 344 ATCCATCCGCTGAGAGAGATAGAGAACTGTGACAGAACTTCAAACTGTTCCTCGAG 403
Db 236 RKVRVVRTRGRMRYNVMVWBTARHRRYNNNGWTBAMAYRRWTMNNNNNNKAMCKRKYW 295

Qy 404 CAAAAGTAGAGTTGATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 463
Db 296 GWNRAVNSTCTTWKSKTKVTRTSWANNCRAGDANKDKHKKWWSAAMGVYVWNNNNNNW 355

Qy 464 AGATTAAGTTCACTACAATCGAGTCTGTGAGCAACTATCAATATGATGATGATGATGAT 523
Db 356 TYKKAHBAARDWVWWSAKWHAHAHAHAYSRKKTBYKRTMNNNNNGTTMWRKMAWYW 415

Qy 524 CCGAGAGAAATCTGATATCTACTTGGAAACAGATGATGATGATGATGATGATGATGATGAT 583
Db 416 KMDMDWBGTYNNNNNGRTYTGKMKMMYYKWKANNCKRWADHKTCTHNNNTTWKMK 475

Qy 584 TGCCACGCTTTCATCATATTCGAATTATTCGATTTGCTCTTTCGATGATGATGATGATGAT 643
Db 476 KTYNNCYWKSMTNGKSHREAAVYTWYMWRRYAHANNNNNDYWKACTWYKYBVCSK 535

Qy 644 ATAAATTCATCTCTCTGGCTTATATCTCACTGATACCGTACGAGCAGCAGCAGCAGCAG 703
Db 536 WNNYAAWYTKSSWNTSYRYRWKTNNSWRWSRSDTRSMGRANNYARABHYGYKWNTRWB 595

Qy 704 AGAGTT 709
Db 596 WSHTWB 601

```

```

RESULT 15
US-09-949-016-12656
; Sequence 12656, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12656
; LENGTH: 253345
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12656

```

```

Query Match      4.4%; Score 38.4; DB 4; Length 253345;
Best Local Similarity 57.5%; Pred. No. 2.6;
Matches 69; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY      438 ATCGAGAGTTGAAGATCTTCCAGCACAGATTAAAGTTCACATAATCGAGTCTGTGAGCA 497
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      17149 ATCATCAGTCTAATATTTTATAGCAAGATTTAAGTTCATTGAAAACTTCCCTATGGAAA 17208

QY      498 ACTATCCAAATATTGATCAGTTCCTATCCGAGAGAAAATCTCGATATCTACTTGGAAACAG 557
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      17209 CACTTCCAATCAAGACCTTACAGCAAGCCCATGAATAAATTAACATTTAAACATGAAAACTG 17268

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Search completed: March 10, 2005, 02:24:01  
Job time : 202 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 22:58:24 ; Search.time 588 Seconds  
(without alignments)  
8789.004 Million cell updates/sec

Title: US-10-612-379-1

Perfect score: 873

Sequence: 1 atggcagaagctaccagat.....ccgatgttaatttcattaa 873

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76.4	8.8	783	13 ADS96405	ADS96405 Drosophil
2	76.4	8.8	1063	4 ABL17133	ABL17133 Drosophil
3	63	7.2	786	3 AAC95377	AAC95377 Cat flea
4	63	7.2	786	3 AAC95376	AAC95376 Cat flea
5	63	7.2	2383	3 AAC95375	AAC95375 Cat flea
6	63	7.2	2383	3 AAC95374	AAC95374 Cat flea
7	51.2	5.9	2000	8 ADA71938	ADA71938 Rice gene
8	48	5.5	2238	11 ADM02307	ADM02307 Human cDN
9	48	5.5	2887	9 ADA24507	ADA24507 Human cDN
10	48	5.5	4290	8 ACC83320	ACC83320 Chloride
11	48	5.5	4318	4 AAK51503	AAK51503 Human pol
12	48	5.5	4318	4 AAI57882	AAI57882 Human pol
13	48	5.5	4318	8 ACF12844	ACF12844 Human cer
14	48	5.5	4318	13 ADR25580	ADR25580 Breast ca
15	48	5.5	4318	13 ADP23232	ADP23232 PRO polyp
16	48	5.5	4707	11 ADM86762	ADM86762 Human cDN
17	46.4	5.3	819	2 AA43260	AA43260 DNA encod
18	46.4	5.3	819	10 ADJ56392	ADJ56392 Human cDN
19	46	5.3	4357	4 AAK52487	AAK52487 Human pol
20	46	5.3	4357	4 AAI59668	AAI59668 Human pol

21	46	5.3	4502	5 AAS87686	AAS87686 DNA encod
22	43.4	5.0	371	8 ABX34992	ABX34992 Bovine ES
23	43.4	5.0	1229	4 AAH02899	AAH02899 Human she
24	43.4	5.0	1652	4 AAI58923	AAI58923 Human pol
25	43.4	5.0	1652	5 ADO99145	ADO99145 DNA encod
26	43.4	5.0	1652	9 ADB48905	ADB48905 Novel hum
27	43.4	5.0	1701	13 ADQ87447	ADQ87447 Human tum
28	43.4	5.0	1713	4 AAI60709	AAI60709 Human pol
29	43.4	5.0	1722	5 ABV29180	ABV29180 Human pro
30	43.4	5.0	1722	5 ABV23328	ABV23328 Human pro
31	43.4	5.0	2260	10 ADB47440	ADB47440 Human cDN
32	43.4	5.0	2662	10 AAD47905	AAD47905 Human tra
33	43	4.9	10560	4 ABL17132	ABL17132 Drosophil
34	42.8	4.9	624	12 ADP28695	ADP28695 Human sec
35	42.8	4.9	859	6 ADI16569	ADI16569 Human NOV
36	42.8	4.9	859	12 ADN42223	ADN42223 Human cDN
37	42.8	4.9	2061	12 ADJ92742	ADJ92742 Human HCL
38	42.8	4.9	2257	12 ADH22598	ADH22598 cDNA enco
39	42.8	4.9	2320	6 ABZ25018	ABZ25018 Laminin B
40	42.8	4.9	2335	10 ADB63066	ADB63066 Human cDN
41	42.8	4.9	2430	6 AAD27280	AAD27280 Human tra
42	42.8	4.9	3389	12 ADH22570	ADH22570 cDNA enco
43	42.8	4.9	3524	12 ADP99220	ADP99220 Human tra
44	42.8	4.9	3641	12 ADJ92727	ADJ92727 Human int
45	41.4	4.7	2000	8 ADA71938	ADA71938 Rice gene

## ALIGNMENTS

### RESULT 1

ADS96405

ID ADS96405 standard; cDNA; 783 BP.

XX AC ADS96405;

XX DT 02-DEC-2004 (first entry)

XX DE Drosophila melanogaster protein coding sequence, SEQ ID 26.

XX KW Insecticide; Antiparasitic; Antihelminthic; gene; ds.

XX OS Drosophila melanogaster.

XX PN WO2004039999-A2.

XX PD 13-MAY-2004.

XX PF 08-AUG-2003; 2003WO-US024982.

XX PR 30-OCT-2002; 2002US-0422377P.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Stam L, Kamdar KP, Spana E, Bachmann J;

XX WPI; 2004-376203/35.

XX DR P-PsDB; ADS96406.

XX PT Identifying a compound that inhibits the activity of a protein for Drosophila viability for use e.g., as insecticidal agent by expressing in a recombinant host a DNA molecule to produce a protein essential for Drosophila viability.

XX PS Claim 1; SEQ ID NO 26; 57pp; English.

XX CC The present invention relates to a method for identifying a compound that inhibits the activity of a protein essential for Drosophila viability. The method comprises: (a) expressing in a recombinant host a DNA sequence encoding a protein essential for Drosophila viability; (b) testing CC compounds suspected of having the ability to inhibit the activity of the protein expressed in (a); and identifying a compound tested in (b) that inhibits the activity of the protein. The method is useful in identifying







519 GATGCCAGGTTACACACATCAGGGTCGGCGCCAGTAATTCGTCGAATTTGAAATTC 578  
 642 ACATAATTTCACTCATCTCTGGGCTTATCTCTCACTGCATACGTCAGCAGCATTTAT 701  
 579 GAGCAATCTAACCGCTTATGCGCTTATATGATATCATCATGATACAGTTGGACGCAATTCAC 638  
 702 TGAGAGTTGTCGCCCGCATCAGGACATTTATCATCTACTATAAGAACAAATGATCTGTT 761  
 639 CCATGCTGCCCGCCAGCCAGACCATATATCATCAACCATATTAACATGCAACAGCAGGAT 698  
 762 CACAAATCAAC 772  
 699 CAGCAATAACC 709

RESULT 5  
 AAC95375/c  
 ID AAC95375 standard; cDNA; 2383 BP.

AAC95375;

19-FEB-2001 (first entry)

Cat flea HMT C1 intracellular channel cDNA complement, SEQ ID NO:1874.

Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;  
 flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis;  
 detection; ss.

Ctenocephalides felis.

WO200061621-A2.

19-OCT-2000.

07-APR-2000; 2000WO-US009437.

09-APR-1999; 99US-0128704P.

(HESK-) HESKA CORP.

Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

WPI; 2000-656323/63.

P-PSDB; AAB29622.

Flea Malpighian tubule and head and nerve cord tissue derived nucleic  
 acids useful for the prevention, diagnosis and treatment of flea  
 infestations.

Claim 1; Page 900-901; 964pp; English.

The invention relates to novel cat flea (Ctenocephalides felis) nucleic  
 acids which are expressed in hindgut and Malpighian tubule (HMT) tissue  
 or head and nerve cord (HNC) tissue. The invention also relates to the  
 encoded proteins. The invention additionally encompasses expression  
 constructs, recombinant viruses and recombinant cells comprising the  
 nucleic acids of the invention, recombinant production of the proteins,  
 antibodies against the proteins, a method of identifying inhibitors of  
 the proteins, and compositions comprising the inhibitors for  
 administration to an animal. The nucleic acids, and the proteins they  
 encode may be used in the prevention, treatment and diagnosis of diseases  
 associated with flea infestations. For example, the nucleic acids may be  
 used to produce an HMT or HNC protein according to standard recombinant  
 DNA methodology by inserting the nucleic acids into a host cell and  
 culturing the cell to express the protein. The HMT and HNC nucleic acids  
 may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect  
 and quantitate the presence of cat flea or other homologous nucleic acid  
 sequences in samples. They may also be used to study the expression and  
 function of the proteins and their role in metabolism. The HMT and HNC  
 proteins may be used as antigens in the production of specific  
 antibodies, and in assays to identify modulators (agonists and  
 antagonists) of HMT and/or HNC protein expression and activity. The anti-

CC HMT/HNC protein antibodies and antagonists may also be used to  
 CC downregulate protein expression and activity. The antibodies may also be  
 CC used as diagnostic agents for detecting the presence of flea polypeptides  
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The  
 CC present sequence represents a cat flea HMT cDNA of the invention  
 XX  
 SQ Sequence 2383 BP; 812 A; 374 C; 354 G; 835 T; 0 U; 8 Other;

Query Match 7.2%; Score 63; DB 3; Length 2383;  
 Best Local Similarity 50.2%; Pred. No. 5.5e-08;  
 Matches 156; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 462 ACAGATTAAAGTTCACTACAATCGAGTCTGTGAGCAACTATCCAATATTGATCAGTTGCT 521  
 Db 1926 AAGGATGACGTAAAGCAATAGTCTGCTGAGCCACCTGAGGAAATCAACGCAATTT 1867  
 Qy 522 ATCCGAGAGAAAAATCTCGATATCTACTTGGAAACAGTATGACTGAATATGACTGTGAAC 581  
 Db 1866 GGCGCGCGCGGCGACGAGATTCCTAACGGGCGACACCATGTGCTTCGACTGCGAACT 1807  
 Qy 582 GATGCCAGTCTTCATCATATTCGAATATTGAATTGATGTCACTCTCTGGATTGATATTC 641  
 Db 1806 GATGCCAGGTTACAAACATCAGGTCGCCGCAAGTATTTTCGTCGAATTTGAAATTC 1747  
 Qy 642 ACATAATTTCACTCATCTCTGGGCTTATATCTCACTGCATACCGTACAGCAGCATTTAT 701  
 Db 1746 GAGCAATCTAACCGCCTTATGCGTTATATGATATCATGTACCATGTGAGCAGCATTCAC 1687  
 Qy 702 TGAGAGTTGTCGCCCGCATCAGGACATTTATCATCACTATAAGAACAAATGATCTGTT 761  
 Db 1686 CCAGTCGTGCCCGCGACCAAGATATCATCAACCATATATAACTGCAACAGCAGGAT 1627  
 Qy 762 CACAAATCAAC 772  
 Db 1626 CAGCAATAACC 1616

RESULT 6  
 AAC95374

ID AAC95374 standard; cDNA; 2383 BP.

AAC95374;

19-FEB-2001 (first entry)

Cat flea HMT C1 intracellular channel cDNA, SEQ ID NO:1872.

Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;  
 flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis;  
 detection; ss.

Ctenocephalides felis.

WO200061621-A2.

19-OCT-2000.

07-APR-2000; 2000WO-US009437.

09-APR-1999; 99US-0128704P.

(HESK-) HESKA CORP.

Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

WPI; 2000-656323/63.

P-PSDB; AAB29622.

Flea Malpighian tubule and head and nerve cord tissue derived nucleic  
 acids useful for the prevention, diagnosis and treatment of flea  
 infestations.

Claim 1; Page 896-898; 964pp; English.



```

Db 550 RCMCYRNGYNTTTSRSMYTKRYKARYTSKRIMYKRYKWCYIYYGMYKCSYMM 491
Qy 611 TTGGATTGTCACCTCTTGGATTGCGATATTCACATAATTCCTCATCTCTGGGCTTATA 670
Db 490 RYGYCKACKCCYAMCWAAGYSGMMYVYKYSKWRMSTKYMSMWYKCRSMKYGAKG 431
Qy 671 TCCTCAGTCATACCGTACAGCAGCATTTATTGAGAGTTGTCGCCGCCGATCAGGACATTA 730
Db 430 CYGCRWYTCYSGYMKWYTYGYSYKYSRCYKYMRYKGMWYMYGWSYSSMMTWYYY 371
Qy 731 TTCATCACTA 740
Db 370 AKYWKYWKYR 361

```

RESULT 8  
ADMO2307  
ID ADMO2307 standard; cDNA; 2238 BP.

XX

AC ADMO2307;

DT 20-MAY-2004 (first entry)

DE Human cDNA of the invention SEQ ID NO:992.

XX ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

PN EPI347046-A1.

PD 24-SEP-2003.

PF 12-APR-2002; 2002EP-00008400.

PR 22-MAR-2002; 2002JP-00137785.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;

DR WPI; 2003-723558/69.

DR P-FSDB; ADM04750.

XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.

PS Claim 1; SEQ ID NO 992; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention may have a use in gene  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC cDNA sequence of the invention.

XX Sequence 2238 BP; 668 A; 440 C; 465 G; 665 T; 0 U; 0 Other;

Query Match 5.5%; Score 48; DB 11; Length 2238;

Best Local Similarity 50.4%; Pred. No. 0.0018;

Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 540 ATATCTACTTGGAAACAGTATGACTGATATGACTGTAATGATGCGCACTTTCATCA 599

Db 637 ATTTCTGATGGCAATGAATGACATTAGCTGATTGCAACCTGCTGCCAACTGCATAT 696

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Qy 600 TATTCGAATTATTCGATTGTCACCTTCTGGATTGCGATATTCACATAATTCATCTCATCT 659
Db 697 TGTCAAGTGTGTGGCCAAAAAATATCGCACTTTGATATTCCTCAAAGAAATGACTGGCAT 756
Qy 660 CTGGGCTTATATCTCTCATCTGATACCGTACAGCAGCATTTATTGAGAGTTGTCGCCGCCGA 719
Db 757 CTGGAGATACCTAACTAATATGATACAGTAGGAGAGTTTACCATACTCTGTCACAGTGA 816
Qy 720 TCAGCAGCATTTATTCATCACTATATAAGAACAAATGAATCTGTTCACAAATCAA 771
Db 817 TAAGAGGTTGAATAGCATATAGTGTAGTGTAGCCAAAAGACTCACCAGTAA 868

```

RESULT 9  
ADA24507

ID ADA24507 standard; cDNA; 2887 BP.

XX ADA24507;

DT 20-NOV-2003 (first entry)

DE Human cDNA differential expressed in adipose tissue, INCYTE1383585.7.

XX ss; differential expression; adipose tissue; cytostatic; hypotensive;  
XX antiarteriosclerotic; antidiabetic; anorectic; gene therapy;  
XX peroxisome proliferator-activated receptor gamma; PPARgamma;  
XX diabetes mellitus; obesity; hypertension; atherosclerosis; breast cancer;  
XX prostate cancer; colon cancer; polycystic ovarian syndrome.

OS Homo sapiens.

XX US2003096272-A1.

XX 22-MAY-2003.

XX 29-JUL-2002; 2002US-00208408.

XX 30-JUL-2001; 2001US-0308868P.

XX (INCY-) INCYTE GENOMICS INC.

XX Schebye XM;

XX WPI; 2003-606416/57.

XX New combination comprising several cDNAs, useful for preparing a  
PT composition for diagnosing or treating diabetes mellitus, obesity,  
PT hypertension, atherosclerosis, or cancer of the breast, prostate or  
PT colon.

PS Claim 1; Page 47-48; 84pp; English.

XX Then invention relates to a new combination comprising 55 cDNAs (ADA24485  
CC -ADA24539) or their complements that are differentially regulated in an  
CC adipose sample. Also included are detecting differential expression of  
CC one or more cDNAs in a sample containing nucleic acids, screening several  
CC molecules or compounds to identify a ligand that specifically binds a  
CC cDNA, a vector comprising the cDNA, a host cell containing the vector,  
CC producing a protein, screening several molecules or compounds, producing  
CC an antibody and the isolated antibody. The cDNAs comprise sequences which  
CC are upregulated or downregulated in response to peroxisome proliferator-  
CC activated receptor gamma (PPARGamma) agonist. The combination comprising  
CC several cDNAs is useful for preparing a composition for diagnosing or  
CC treating diabetes mellitus, obesity, hypertension, atherosclerosis,  
CC cancer of the breast, prostate or colon, or polycystic ovarian syndrome.

XX Sequence 2887 BP; 872 A; 552 C; 560 G; 903 T; 0 U; 0 Other;

Query Match 5.5%; Score 48; DB 9; Length 2887;

Best Local Similarity 50.4%; Pred. No. 0.002;

Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy	540	ATATCTACTTGGAAACAGTATGACATGGAATATGACTGTGGAATGCAAGTATGCCAGTCTTTCATCA	599
Db	816	ATTTCCTGGATGGCAATGAAATGACATATTAGCTGATTTGCAACCTGCTGCCCAAACTGCATAT	875
Qy	600	TATTCCGAATTATTGGATTGTCTCACTCTCTTGGATATTCGATATTCGATATTCACATAATTTTCATCTCATCT	659
Db	876	TGTCAAGGTGGTGGCCAAAATAATCGCAACTTTTGATATTCCAAAGAAATGACTGGCAT	935
Qy	660	CTGGGCTTATATCTCTCACTGTCATACCGTACAGCAGCATTTATTTCAGAGTTGTCTCCGCCGA	719
Db	936	CTGGAGATACCTTAACATATGCATACAGTAGGACGAGTTACCAATACCTGTGCCAGTGA	995
Qy	720	TCAGGACATATTTCATCACTATAAGAAACAAATGAATCTGTTCACAAATCAA	771
Db	996	TAAAGAGTTGAAATAGCATATAGTGTAGTGTAGCCAAAAGACTCTACCAAGTAA	1047

RESULT 10	
ACC83320	
ID	ACC83320 standard; DNA; 4290 BP.
XX	
AC	ACC83320;
XX	
DT	22-AUG-2003 (first entry)
XX	
DE	Chloride intracellular channel 4 gene #SEQ ID 2.
XX	
KW	NP-ATC isoform a; chloride intracellular channel 4; osteopathic;
KW	antiarthritic; antidiabetic; nephrotropic; osteoclast;
KW	bone metabolic marker; arthritis; osteoporosis; arthritis deformans;
KW	systemic erythematodes; bone reduction; diabetes; renal failure; gene;
ds.	
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
CDS	198..959
FT	/*tag= a
FT	/product= "chloride intracellular channel 4"
FT	
XX	
PN	WO2003027284-A1.
XX	
PD	03-APR-2003.
XX	
PF	25-SEP-2002; 2002WO-JP009882.
XX	
PR	26-SEP-2001; 2001JP-00294804.
PR	10-MAY-2002; 2002JP-00136030.
XX	
PA	(SUMU ) SUMITOMO PHARM CO LTD.
PA	(TAKE/) TAKEYA T.
XX	
PI	Takeya T, Hayashi K;
XX	
DR	WPI; 2003-393338/37.
DR	P-PSDB; ABR62135.
XX	
PT	Bone metabolic disease marker and encoded polynucleotide for accelerated differentiation/activation of osteoclasts, applicable in diagnosis of screening drugs for treating e.g. arthritis and osteoporosis.
PT	
XX	
PS	Claim 1; Page 61-63; 78pp; Japanese.
XX	
CC	The invention relates to a bone metabolic marker associated with the accelerated differentiation or activation of osteoclasts. This consists of a polynucleotide having not less than 15 consecutive bases in the sequence of the NP-ATC isoform a gene, or that of the chloride intracellular channel 4 gene. The protein and its encoded polynucleotide are applicable in diagnosis of and screening drugs for e.g. arthritis, osteoporosis, arthritis deformans, systemic erythematodes, bone reduction in diabetes and reduction of bone density in chronic renal failure. The current sequence represents the chloride intracellular channel 4 gene
XX	

SQ Sequence 4290 BP; 1287 A; 764 C; 832 G; 1407 T; 0 U; 0 Other;  
 Query Match 5.5%; Score 48; DB 8; Length 4290;  
 Best Local Similarity 50.4%; Pred. No. 0.0024;  
 Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
 Qy 540 ATATCTACTTGGAAACAGTATGACTGAATATGACTGTGAACCTGATGCCACGCTTTCATCA 599  
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 728 ATTCTCGATGGCAATGAAATGACATTAGCTGATTGCAACCTGCTGCCAAACTGCATAT 787  
 Qy 600 TATTGCAATATTGGATTGTGCTCTTCTTGATTCGATATTCCACATATTTTCACTCATCT 659  
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 788 TGTCAAGGTGGTGGCCAAAAATATCGCAACTTTGTATATTTCCAAAAGAAATGACTGGCAT 847  
 Qy 660 CTGGGCTTATATCTCTCACTGCATACCTGACAGCAGCATTTATTGAGAGTTGTCTCCGCCGA 719  
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 848 CTGAGATACCTAACTAATGTCATACAGTAGGGACGAGTTCCACCAATACCTGTCCAGTGA 907  
 Qy 720 TCAGGACATATTTCATCATCTATTAAAGAACAAATGAATCTCTTCACAATCAA 771  
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 908 TAAGGAGTTGAAATAGCATATAGTGATGTAGTGCACCAAAAGACTCACCAAGTAA 959  
 RESULT 11  
 AAKS1503  
 ID AAKS1503 standard; cDNA; 4318 BP.  
 XX  
 AC AAKS1503;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 48.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US004098.  
 XX  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 PR 20-JUN-2000; 2000US-00598075.  
 PR 19-JUL-2000; 2000US-00620325.  
 PR 01-SEP-2000; 2000US-00654936.  
 PR 15-SEP-2000; 2000US-00663561.  
 PR 20-OCT-2000; 2000US-00699325.  
 PR 30-NOV-2000; 2000US-00728422.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX  
 WI: 2001-476283/51.  
 DR P-PSDB; AAM78370.  
 XX  
 CC Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.  
 PT  
 PS Claim 1; Page 622-625; 6221pp; English.  
 PS  
 CC The invention relates to polynucleotides (AAKS15456-AAKS3435) and the  
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, hematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX

XX SQ Sequence 4318 BP; 1319 A; 769 C; 814 G; 1416 T; 0 U; 0 Other;

Query Match 5.5%; Score 48; DB 4; Length 4318;  
Best Local Similarity 50.4%; Pred. No. 0.0024;  
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 540 ATATCTACTTGGAAACAGTATGACTGAATATGACTGTGCACTGATGCCACGCTTTCATCA 599  
DB 697 ATTTCTGGATGGCAATGAAATGACATTAGCTGATTGCAACCTGCTGCCAAACTGCATAT 756  
QY 600 TATTCGAATTATTGATGTGCTACTTCTGGATTGATATTCACATATTTCACTCATCT 659  
DB 757 TGTCAAGTGGTGGCCAAAATAATATGCAACTTTGATATTTCCAAAGAAATGACTGGCAT 816  
QY 660 CTGGGCTTATATCTCTCACTGCATACCGTACAGCAGCAATTTATTGAGAGTGTGCCGCCGA 719  
DB 817 CTGGAGATACCTAATGATATGATAGTAGGAGCAGTTCACCAATACCTGTCCCAAGTGA 876  
QY 720 TCAGGACATTTATCATCTACTATAAAGAACAAATGAATCTGTTCAAAATCAA 771  
DB 877 TAAGGAGTTGAAATAGCATATAGTGATGTAGCCAAAGAGCTCACCAGTAA 928

RESULT 12

AAI57882  
ID AAI57882 standard; cDNA; 4318 BP.

XX AAI57882;

DT 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 85.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
XX leukaemia; ss.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00682191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
XX Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.  
XX P-PSDB; AAM38726.

XX Novel nucleic acids and polypeptides, useful for treating disorders such  
XX as central nervous system injuries.

XX Claim 1; SEQ ID NO 85; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
XX encoded polypeptides (AAM38642-AAM42213) with nontropic,  
XX immunosuppressant and cytostatic activity. The polynucleotides are useful  
XX in gene therapy. A composition containing a polypeptide or polynucleotide  
XX of the invention may be used to treat diseases of the peripheral nervous  
XX system, such as peripheral nervous injuries, peripheral neuropathy and  
XX localised neuropathies and central nervous system diseases, such as  
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
XX utilisation of the activities such as: Immune system suppression,  
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
XX assays for receptor activity, arthritis and inflammation, leukaemias and  
XX C.N.S disorders. Note: The sequence data for this patent did not form  
XX part of the printed specification

XX SQ Sequence 4318 BP; 1319 A; 769 C; 814 G; 1416 T; 0 U; 0 Other;

Query Match 5.5%; Score 48; DB 4; Length 4318;  
Best Local Similarity 50.4%; Pred. No. 0.0024;  
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 540 ATATCTACTTGGAAACAGTATGACTGAATATGACTGTGCACTGATGCCACGCTTTCATCA 599  
DB 697 ATTTCTGGATGGCAATGAAATGACATTAGCTGATTGCAACCTGCTGCCAAACTGCATAT 756  
QY 600 TATTCGAATTATTGATGTGCTACTTCTGGATTGATATTCACATATTTCACTCATCT 659  
DB 757 TGTCAAGTGGTGGCCAAAATAATGCAACTTTGATATTTCCAAAGAAATGACTGGCAT 816  
QY 660 CTGGGCTTATATCTCTCACTGCATACCGTACAGCAGCAATTTATTGAGAGTGTGCCGCCGA 719  
DB 817 CTGGAGATACCTAATGATATGATAGTAGGAGCAGTTCACCAATACCTGTCCCAAGTGA 876  
QY 720 TCAGGACATTTATCATCTACTATAAAGAACAAATGAATCTGTTCAAAATCAA 771  
DB 877 TAAGGAGTTGAAATAGCATATAGTGATGTAGCCAAAGAGCTCACCAGTAA 928

RESULT 13

ACF12844  
ID ACF12844 standard; cDNA; 4318 BP.

XX ACF12844;

XX 10-SEP-2003 (first entry)

XX Human cervical cancer cell marker encoding cDNA SEQ ID NO:33.

XX Human; cervical cancer; cervical cancer marker; cancer therapy;  
XX detection; gene therapy; vaccine; gene; ss.

XX Homo sapiens.

XX WO2002101075-A2.

XX 19-DEC-2002.

XX 12-JUN-2002; 2002WO-US018638.

XX 13-JUN-2001; 2001US-0298155P.

XX 13-JUN-2001; 2001US-0298159P.

XX 14-NOV-2001; 2001US-0335936P.

XX

PA (MILL-) MILLENNIUM PHARM INC.  
XX Schlegel R, Chen Y, Zhao X, Monahan JF, Kamatkar S;  
PI Ganavarapu M, Glatk K, Hoersch S;  
XX WPI: 2003-156967/15.  
DR P-PSDB; ABR92063.  
XX New isolated nucleic acid molecule useful for detecting, characterizing,  
PT preventing and treating human cervical cancers, in various prognostic and  
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.  
XX Claim 4; Page 160-161; 386pp; English.  
XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)  
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than  
CC normal indicates the presence of cervical cancer. Also described: (1) a  
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)  
CC assessing (MI) whether a patient is afflicted with cervical cancer,  
CC comprising comparing the level of expression of a marker in a patient's  
CC sample, and the normal level of expression of the marker in a control non  
CC -cervical cancer sample, where a significant increase in the level of  
CC expression of the marker in the patient's sample relative to that in the  
CC control sample is an indication that the patient is afflicted with  
CC cervical cancer. (I) has cytostatic activity, and can be used in gene  
CC therapy and in vaccines. (I) is useful in detecting, characterizing,  
CC preventing and treating human cervical cancers. (I) may also be used in  
CC various prognostic and diagnostic assays, pharmacogenomics and in  
CC monitoring clinical trials  
XX Sequence 4318 BP; 1315 A; 764 C; 832 G; 1407 T; 0 U; 0 Other;  
SQ Query Match 5.5%; Score 48; DB 8; Length 4318;  
Best Local Similarity 50.4%; Pred. No. 0.0024;  
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 540 ATATCTACTTGGAAACAGTATGACTGGAATATGACTGTGAACTGATGCGCACGCTTTCATCA 599  
Db 728 ATTTCTGGATGGCAATGAAATGACATTAGCTGATTCGCAACCTGCTGCCCAAACTGCATAT 787  
QY 600 TATTCGAAATATTGGATTGTCACTTCTTGGATTTCGATATTCACATAATTTCACTCATCT 659  
Db 788 TGTCAAGGTGGTGGCCAAATAATATCGCAACTTTTGATATTCGCAAAAGAAATGACTGGCAT 847  
QY 660 CTGGCTTATATCTCACTGATACCGTACAGCAGCATTTATTGAGAGTTGTCCCGCGCA 719  
Db 848 CTGGAGATACCTAATAATGATATGATAGGAGCAGGTTCCACCATACCTGTGCCAGTGA 907  
QY 720 TCAGGACATTATTCATCACTATAAAGAACAAATGAATCTGTTCACAAAATCAA 771  
Db 908 TAAGGAGGTTGAAATAGCATATAGTATGATGATGAGGAGGAGTTCCCAATACCTGTCCCAAGTAA 959  
RESULT 14  
ADR25580  
ID ADR25580 standard; DNA; 4318 BP.  
XX ADR25580;  
XX 21-OCT-2004 (first entry)  
DT Breast cancer prognosis marker #1441.  
DE Breast cancer; prognosis; gene expression; diagnosis.  
KW Homo sapiens.  
OS WO2004065545-A2.  
PN 05-AUG-2004.  
PD 15-JAN-2004; 2004WO-US001100.  
XX 15-JAN-2003; 2003US-00342887.  
XX (ROSE-) ROSETTA INPHARMATICS LLC.  
XX (NECA-) NETHERLANDS CANCER INST.  
XX Van't Veer LJ, He Y;  
XX WPI: 2004-593473/57.  
XX Classifying a breast cancer patient according to prognosis comprises  
PT determining the similarity between the level of expression of each of  
PT five genes in a cell sample taken from patient, to control levels.  
XX Disclosure; SEQ ID NO 1441; 226pp; English.  
XX The invention relates to a method of classifying a breast cancer patient  
CC according to prognosis by determining the similarity between the level of  
CC expression of each of five genes for which markers are listed in the  
CC specification, in a cell sample taken from the breast cancer patient, to  
CC control levels of expression for each respective five genes to obtain a  
CC patient similarity value. The methods are useful for classifying a breast  
CC cancer patient according to prognosis. Kits and computer program products  
CC are useful for data analysis using the diagnostic, prognostic and  
CC statistical methods of the invention. This sequence corresponds to a  
CC marker used in the method of the invention.  
XX Sequence 4318 BP; 1315 A; 764 C; 832 G; 1407 T; 0 U; 0 Other;  
SQ Query Match 5.5%; Score 48; DB 13; Length 4318;  
Best Local Similarity 50.4%; Pred. No. 0.0024;  
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 540 ATATCTACTTGGAAACAGTATGACTGGAATATGACTGTGAACTGATGCGCACGCTTTCATCA 599  
Db 728 ATTTCTGGATGGCAATGAAATGACATTAGCTGATTCGCAACCTGCTGCCCAAACTGCATAT 787  
QY 600 TATTCGAAATATTGGATTGTCACTTCTTGGATTTCGATATTCACATAATTTCACTCATCT 659  
Db 788 TGTCAAGGTGGTGGCCAAATAATATCGCAACTTTTGATATTCGCAAAAGAAATGACTGGCAT 847  
QY 660 CTGGCTTATATCTCACTGATACCGTACAGCAGCATTTATTGAGAGTTGTCCCGCGCA 719  
Db 848 CTGGAGATACCTAATAATGATATGATAGGAGCAGGTTCCACCATACCTGTGCCAGTGA 907  
QY 720 TCAGGACATTATTCATCACTATAAAGAACAAATGAATCTGTTCACAAAATCAA 771  
Db 908 TAAGGAGGTTGAAATAGCATATAGTATGATGATGAGGAGGAGTTCCCAATACCTGTCCCAAGTAA 959  
RESULT 15  
ADP23232  
ID ADP23232 standard; cDNA; 4318 BP.  
XX ADP23232;  
XX 18-NOV-2004 (first entry)  
DT PRO polypeptide encoding cDNA SEQ ID NO:326.  
DE ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
KW immunosuppressive; osteopathic; antidiabetic; dermatological;  
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
KW gene therapy; immune system.  
XX Unidentified.  
OS WO2004041170-A2.  
PN 21-MAY-2004.  
PD 30-OCT-2003; 2003WO-US034312.  
PF 01-NOV-2002; 2002US-0423394P.  
PR

Thu Mar 10 08:34:29 2005

XX (GETH ) GENENTECH INC.  
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
XX Wu TD;  
XX WPI; 2004-419628/39.  
XX P-P5DB; ADF23233.  
XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
XX renal disease, or demyelinating diseases of the central or peripheral  
XX nervous system.  
XX Claim 1; SEQ ID NO 326; 2940pp; English.  
XX The invention relates to a novel isolated nucleic acid and the PRO  
XX polypeptide encoded by it. A protein of the invention has  
XX antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,  
XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
XX of the invention may have a use in gene therapy. The PRO polypeptide, its  
XX agonist, antagonist, or antibody that specifically binds to the  
XX polypeptide is useful for treating an immune related disorder such as  
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
XX disease, a demyelinating disease of the central or peripheral nervous  
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
XX disease, infectious or autoimmune chronic active hepatitis, primary  
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
XX disease, asthma, allergic rhinitis, atopic dermatitis, food  
XX hypersensitivity, urticaria, an immunologic disease of the lung,  
XX eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
XX pneumonitis, a transplantation associated disease, graft rejection or  
XX graft-versus-host disease. The present sequence encodes a PRO protein of  
XX the invention.  
XX Sequence 4318 BP; 1315 A; 764 C; 832 G; 1407 T; 0 U; 0 Other;  
SQ

Query Match 5.5%; Score 48; DB 13; Length 4318;  
Best Local Similarity 50.4%; Pred. No. 0.0024;  
Matches 117; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 540 ATATCTACTTGGAAACAGTATGACTCAATATGACTGTGAACGTGCCACGCTTTCATCA 599  
DB 728 ATTCTGGATGGGAATGAATGACATTAGCTGTGCAACCTGCTGCCAACTGCATAT 787  
QY 600 TATTCGAATTATTTGGATTCTCTTGGATTTCGATATTCACATAATTTCACTCATCT 659  
DB 788 TGTCAGAGTGGTGGCCAAAATATCGCAACTTTGATATTCAAAAGAAATGACTGGCAT 847  
QY 660 CTGGGCTTATCTCTCACTGCATACCGTACAGCAGCATTTATGAGAGTTGTCGCCGGA 719  
DB 848 CTGGAGATACCTAACTAATGTCATACAGTAGGACGAGTTTACCAATACCTGTCCAGTGA 907  
QY 720 TCAGGACATTTATCATCATATAAGAACAAATGATCTGTTTCAAAATCAA 771  
DB 908 TAAGGAGGTTGAATAGCATATAGTGTAGCCAAAGACTCACCAGTAA 959

Search completed: March 10, 2005, 00:12:31  
Job time : 595 secs